

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2005, 15:12:44 ; Search time 175 Seconds
(without alignments)
471.113 Million cell updates/sec

Title: US-10-758-210-6

Perfect score: 161
Sequence: 1 AGSRKANIGRRRRRTALAG.....ANNVYKQYEDMVVEACGR 161

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 6

Total number of hits satisfying chosen parameters: 14555

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_tramb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	161	100.0	461 1 GDF7 MOUSE	P43029 mus musculus
2	97	60.2	294 2 G9BDW8	Q9BDW8 macaca fasc
3	97	60.2	447 1 GDF7_CERAE	Q9BDW8 cercopithec
4	69	42.9	450 1 GFD7_HUMAN	Q724P5 homo sapien
5	69	42.9	453 2 G75RY1	Q75RY1 homo sapien
6	67	41.6	67 2 O02784	O02784 bos taurus
7	50	31.1	7 2 O8K4X3	O8K4X3 rattus norv
8	44	27.3	126 2 O93573	O93573 gallus gall
9	44	27.3	413 2 Q9DGM4	Q9DGM4 xenopus lae
10	31	19.3	79 2 Q91700	Q91700 xenopus lae
11	29	18.0	67 2 O8K4X4	O8K4X4 rattus norv
12	29	18.0	125 1 GDF6 MOUSE	P43028 mus musculus
13	29	18.0	201 2 O6P158	O6P158 homo sapien
14	29	18.0	436 1 GDF6_BOVIN	P51106 bos taurus
15	29	18.0	452 2 O6HA10	O6HA10 rattus norv
16	29	18.0	454 2 Q70UT4	Q70UT4 mus musculus
17	29	18.0	455 2 O6KFI0	O6KFI0 homo sapien
18	25	15.5	399 2 Q9W753	Q9W753 xenopus lae
19	23	14.3	261 2 O9W6C0	O9W6C0 brachydanto
20	22	13.7	165 2 O95UX1	O95UX1 drosophila
21	22	13.7	166 2 Q95UX0	Q95UX0 drosophila
22	22	13.7	207 2 Q43522	Q43522 lycopersico
23	22	13.7	336 2 Q7Q8W9	Q7Q8W9 anopheles g
24	21	13.0	163 2 Q95UM7	Q95UM7 drosophila
25	21	13.0	239 2 O69T79	O69T79 oryza sativ
26	21	13.0	267 2 O6D112	O6D112 xenopus tro
27	21	13.0	271 2 O49216	O49216 oryza sativ
28	21	13.0	272 2 O49228	O49228 oryza sativ
29	21	13.0	272 2 Q7F3M4	Q7F3M4 oryza sativ
30	21	13.0	321 2 O69XV3	O69XV3 oryza sativ
31	21	13.0	541 2 O87BZ7	O87BZ7 xylella fas

32	21	13.0	673 2 O653C5	O653C5 oryza sativ
33	21	13.0	1504 2 Q7PSM9	Q7PSM9 anopheles g
34	21	13.0	1868 2 Q9WMP3	Q9WMP3 drosophila
35	20	12.4	61 2 O8RJA2	O8RJA2 xanthomonas
36	20	12.4	93 2 O6Y122	O6Y122 oryza sativ
37	20	12.4	106 2 Q9GP80	Q9GP80 drosophila
38	20	12.4	118 2 Q9VY86	Q9VY86 drosophila
39	20	12.4	155 2 Q9GND8	Q9GND8 drosophila
40	20	12.4	155 2 O9GP74	O9GP74 drosophila
41	20	12.4	156 2 O9GNB7	O9GNB7 drosophila
42	20	12.4	156 2 Q9GP73	Q9GP73 drosophila
43	20	12.4	157 2 Q9GP77	Q9GP77 drosophila
44	20	12.4	159 2 Q95UW1	Q95UW1 drosophila
45	20	12.4	159 2 Q95UW5	Q95UW5 drosophila

ALIGNMENTS

RESULT 1
GDF7_MOUSE STANDARD; PRT; 461 AA.
ID GDF7_MOUSE
AC P43029; Q7TNX4; Q99WY1;
DT 01-NOV-1995 (Rel. 32, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Growth/differentiation factor 7 precursor (GDF-7).
GN Name=Gdf7; Synonyms=Gdf-7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=BALB/c; TISSUE=Testis;
RA Guo J.H., Yu L.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE OF 1-441 FROM N.A. (ISOFORM 1).
RC STRAIN=TT2;
RA Watakabe A., Fujita H., Hayaishi M., Yamamori T.;
RL MEDLINE=94195427; PubMed=8145850; DOI=10.1038/368639a0;
RA Storm B.E., Huynh T.V., Copeland N.G., Jenkins N.A., Kingstley D.M.,
RT "Limb alterations in brachypodism mice due to mutations in a new
member of the TGF beta-superfamily.";
RL Nature 368:639-643(1994).
[3]
RN SEQUENCE OF 311-461 FROM N.A.
RC STRAIN=BALB/c; TISSUE=Liver;
RA MEDLINE=94195427; PubMed=8145850; DOI=10.1038/368639a0;
RA Storm B.E., Huynh T.V., Copeland N.G., Jenkins N.A., Kingstley D.M.,
RT "Limb alterations in brachypodism mice due to mutations in a new
member of the TGF beta-superfamily.";
RL Nature 368:639-643(1994).
[4]
RN SUBUNIT: Homodimer; disulfide-linked (By similarity).
[5]
RN ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=1;
IsoId=P43029-1; Sequence=Displayed;
Name=2;
IsoId=P43029-2; Sequence=VSP_010764;
[6]
RN SIMILARITY: Belongs to the TGF-beta family.
[7]
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[8]
EMBL: AF525752; AAP97721.1; -
EMBL: AF254571; AKK30843.1; -

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DR EMBL; AF254570; AAK30843.1; JOINED.
DR EMBL; U08339; AAA18780.1; -.
DR PIR; S43296; S43296.
DR HSSP; P12643; 3BMP.
DR MGD; MG1:95890; Gdf7.
DR GO; GO:0005576; C:extracellular; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007411; P:axon guidance; IDA.
DR InterPro; IPR002405; GF_cyskn0t.
DR InterPro; IPR002400; Inhibin_alpha.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF_beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
DR Alternative splicing; Cytokine; Glycoprotein; Growth factor; Signal.
KW SIGNAL
FT SIGNAL 1 19 potential.
FT PROPEP 20 315 potential.
FT CHAIN 316 461 Growth/differentiation factor 7.
FT DISULFID 360 426 By similarity.
FT DISULFID 389 458 By similarity.
FT DISULFID 393 460 By similarity.
FT DISULFID 425 425 Interchain (By similarity).
FT DOMAIN 311 315 Poly-Arg.
FT DOMAIN 326 351 Poly-Gly.
FT CARBOHYD 79 79 N-linked (GlcNAc...) (Potential).
FT VARSPIC 123 130 Missing (in isoform 2).
SQ SEQUENCE 461 AA; 47890 MW; 92C2511C86DE478 CRC64;

Query Match 100.0%; Score 161; DB 1; Length 461;
Best local Similarity 100.0%; Pred. No. 1,1e-140;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGSRKANLVGRRRRRTALAGTRGAQSGGGGGGGGGGGGGAGRGHGRGRSRC 60
DB 301 AGSRKANLVGRRRRRTALAGTRGAQSGGGGGGGGGGGGGAGRGHGRGRSRC 360

QY 61 SRSLHVDPELGDWDWIIPLDVEAHGCGVDFPRLSHLEPTNNAIIQTLLNSMAPDA 120
DB 361 SRSLHVDPELGDWDWIIPLDVEAHGCGVDFPRLSHLEPTNNAIIQTLLNSMAPDA 420

QY 121 APASCCVPARLSPISILYIDANNVVKQYEDMVVEACGR 161
DB 421 APASCCVPARLSPISILYIDANNVVKQYEDMVVEACGR 461

RESULT 2
Q9BDM9 PRELIMINARY; PRT; 294 AA.
ID Q9BDM9
AC Q9BDM9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Growth/differentiation factor 7 (Fragment).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Ctenista; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OC NCBI_TaxID=9541;
OX [1]
RN SOURCE FROM N.A.
RP TISSUE=Cerebral cortex motor area;
RA MEDLINE=21136583; PubMed=1128730;
RA Metakabe A., Fujita H., Hayashi M., Yamamori T.;
RT "Growth/differentiation factor 7 is preferentially expressed in the
RT primary motor area of the monkey neocortex.";
RL J. Neurochem. 76:1455-1464(2001)
CC -1- SIMILARITY: Belongs to the TGF-beta family.
DR EMBL; AF254567; AAK27794.1; -.
DR HSSP; P12643; 3BMP.
DR GO; GO:0008083; F:growth factor activity; IEA.

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DR InterPro; IPR002400; GF_cyskn0t.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF_beta; 1.
DR PRINTS; PR00438; GFCYSKN0T.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor.
FT NON TER 1 1
SQ SEQUENCE 294 AA; 31792 MW; 49B7BCD9F27A93F CRC64;

Query Match 60.2%; Score 97; DB 2; Length 294;
Best local Similarity 100.0%; Pred. No. 1,7e-81;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 LHVDFPELGDWDWIIPLDVEAHGCGVDFPRLSHLEPTNNAIIQTLLNSMAPDAAPS 124
DB 198 LHVDFPELGDWDWIIPLDVEAHGCGVDFPRLSHLEPTNNAIIQTLLNSMAPDAAPS 257

QY 125 CCVPARLSPISILYIDANNVVKQYEDMVVEACGR 161
DB 258 CCVPARLSPISILYIDANNVVKQYEDMVVEACGR 294

RESULT 3
GDF7_CERAE
ID GDF7_CERAE STANDARD; PRT; 447 AA.
AC Q9BDM9;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Growth/differentiation factor 7 precursor (GDF-7).
GN Name=GDF7;
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OC NCBI_TaxID=9534;
OX [1]
RN SOURCE FROM N.A. AND TISSUE SPECIFICITY.
RA MEDLINE=21136583; PubMed=1128730;
RA Metakabe A., Fujita H., Hayashi M., Yamamori T.;
RT "Growth/differentiation factor 7 is preferentially expressed in the
RT primary motor area of the monkey neocortex.";
RL J. Neurochem. 76:1455-1464(2001)
CC -1- FUNCTION: May play an active role in the motor area of the primate
CC neocortex.
CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -1- TISSUE SPECIFICITY: Highly expressed in the primary area of brain
CC neocortex.
CC -1- SIMILARITY: Belongs to the TGF-beta family.
CC -----
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CC -----
DR EMBL; AF254569; AAK30842.1; -.
DR EMBL; AF254568; AAK30842.1; JOINED.
DR HSSP; P12643; 3BMP.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF_beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 19 potential.
FT PROPEP 20 318 potential.

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FT CHAIN 319 447 Growth/differentiation factor 7.
 FT DISUP.FID 346 412 By similarity.
 FT DISUP.FID 375 444 By similarity.
 FT DISUP.FID 379 446 By similarity.
 FT DISUP.FID 411 411 Interchain (By similarity).
 FT CARBOHYD 80 80 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 447 AA; 46866 MW; DF46D591925A8391 CRC64;

Query Match 60.2%; Score 97; DB 1; Length 447;
 Best Local Similarity 100.0%; Pred. No. 2.4e-81;
 Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 LHVDPKELGMDWIIAPLDYEAHCEGVCDFPLRSHLEPTNHAIIQTLNSMAPDAPAS 124
 DB 351 LHVDPKELGMDWIIAPLDYEAHCEGVCDFPLRSHLEPTNHAIIQTLNSMAPDAPAS 410

QY 125 CCVPARLSPISILYIDANNVVKQYEDMVEACGCR 161
 DB 411 CCVPARLSPISILYIDANNVVKQYEDMVEACGCR 447

RESULT 4
 GPD7_HUMAN STANDARD; PRT; 450 AA.
 ID GPD7_HUMAN
 AC Q7Z4P5;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Growth/differentiation factor 7 precursor (GDF-7).
 GN Name=GDF7;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Guo J.H., Yu L.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: May play an active role in the motor area of the primate
 CC neocortex (By similarity).
 CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
 CC -----
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CC EMBL; AF522369; AAP97720.1; -;
 CC Genew; HGNC:4222; GDF7.
 CC MIM; 604651; -;
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00019; TGF_beta; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Cytochrome; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 19 Potential.
 FT PROPEP 20 321 Potential.
 FT CHAIN 322 450 Growth/differentiation factor 7.
 FT DISUP.FID 349 415 By similarity.
 FT DISUP.FID 378 447 By similarity.
 FT DISUP.FID 382 449 By similarity.
 FT DISUP.FID 414 414 Interchain (By similarity).
 FT CARBOHYD 83 83 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 450 AA; 46966 MW; CDB4C617685D37BD CRC64;

Query Match 42.9%; Score 69; DB 1; Length 450;
 Best Local Similarity 100.0%; Pred. No. 2.2e-55;
 Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 CDEPLSHLEPTNHAIIQTLNSMAPDAPASCCVPARLSPISILYIDANNVVKQYED 152
 DB 385 CDEPLSHLEPTNHAIIQTLNSMAPDAPASCCVPARLSPISILYIDANNVVKQYED 444

QY 153 MVEACGCR 161
 DB 445 MVEACGCR 450

RESULT 5
 Q75RY1 PRELIMINARY; PRT; 453 AA.
 ID Q75RY1
 AC Q75RY1;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Growth differentiation factor 7.
 GN Name=gdf7;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Suzuki M., Shimokawa H., Kasugai S.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
 DR EMBL; AB158468; BAD07014.1; -;
 DR HSP; P01137; IRLA.
 DR GO; GO:0008083; F: growth factor activity; IEA.
 DR GO; GO:0040007; P: growth; IEA.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR Pfam; PF00019; TGF_beta; 1.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Growth factor.
 SQ SEQUENCE 453 AA; 47121 MW; 9FD8CB759C63DPID CRC64;

Query Match 42.9%; Score 69; DB 2; Length 453;
 Best Local Similarity 100.0%; Pred. No. 2.2e-55;
 Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 CDEPLSHLEPTNHAIIQTLNSMAPDAPASCCVPARLSPISILYIDANNVVKQYED 152
 DB 385 CDEPLSHLEPTNHAIIQTLNSMAPDAPASCCVPARLSPISILYIDANNVVKQYED 444

QY 153 MVEACGCR 161
 DB 445 MVEACGCR 450

RESULT 6
 Q02784 PRELIMINARY; PRT; 67 AA.
 ID Q02784
 AC Q02784;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Growth differentiation factor-7 (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.

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RX MEDLINE=98183403; PubMed=9514880; DOI=10.1006/bbrc.1998.8213;
RA Morome Y., Goseki-Sone M., Ishikawa I., Oida S.;
RT "Gene expression of growth and differentiation factors-5, -6, and -7
in developing bovine tooth at the root forming stage.";
RL Biochem. Biophys. Res. Commun. 244:85-90(1998).
CC -1- SIMILARITY: Belongs to the TGF-beta family.
DR EMBL; AB004302; BAA20364.1; -.
DR HSSP; P12643; 1ES7.
DR GO; GO:0008083; F: growth factor activity; IEA.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF_beta; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR Growth factor.
KM NON_TER 1 1
FT NON_TER 67 67
SQ SEQUENCE 67 AA; 7286 MW; 37B5EA34CDA80D9 CRC64;

Query Match 41.6%; Score 67; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 3.2e-54;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 PLDYEAHCGVCDFPLRSHLEPTNHAIIQTLNSMAPDAAPASCVPARLSPISILYID 140
DB 1 PLDYEAHCGVCDFPLRSHLEPTNHAIIQTLNSMAPDAAPASCVPARLSPISILYID 60

QY 141 AANNVY 147
DB 61 AANNVY 67

RESULT 7
08K4X3 PRELIMINARY; PRT; 67 AA.
AC 08K4X3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Growth and differentiation factor-7 (Fragment).
GN Name=gdf-7;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Oida S., Morome Y., Nakamura T., Terahima T.;
RT "Molecular Cloning of PCR Amplified BMP-Related Genes (GDF-5, 6 and 7)
from Rat Tooth Cells Using Modified pBluescript SK+ Vector.";
RL Journal of hard tissue biology 6:16-20(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Oida S., Sema K.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
CC -1- SIMILARITY: Belongs to the TGF-beta family.
DR EMBL; AB087406; BAC02715.1; -.
DR HSSP; P12643; 1ES7.
DR GO; GO:0008083; F: growth factor activity; IEA.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF_beta; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR Growth factor.
KM NON_TER 1 1
FT NON_TER 67 67
SQ SEQUENCE 67 AA; 7292 MW; 3AD88A24CDA81579 CRC64;

Query Match 31.1%; Score 50; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 1.8e-38;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 PLDYEAHCGVCDFPLRSHLEPTNHAIIQTLNSMAPDAAPASCVPAR 130

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DB 1 PLDYEAHCGVCDFPLRSHLEPTNHAIIQTLNSMAPDAAPASCVPAR 50

RESULT 8
093573 PRELIMINARY; PRT; 126 AA.
AC 093573;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative growth/differentiation factor 6/7 (fragment).
GN Name=gdf6/7;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99026113; PubMed=9808626;
RA Lee K.J., Mendelsohn M., Jessell T.M.;
RT "Neuronal patterning by BMPs: a requirement for GDF7 in the generation
of a discrete class of commissural interneurons in the mouse spinal
cord.";
RL Genes Dev. 12:3394-3407(1998).
CC -1- SIMILARITY: Belongs to the TGF-beta family.
DR EMBL; AF089086; AAC97113.1; -.
DR HSSP; P08476; 1NVU.
DR GO; GO:0005576; C: extracellular; IEA.
DR GO; GO:0008083; F: growth factor activity; IEA.
DR GO; GO:0008151; P: cell growth and/or maintenance; IEA.
DR InterPro; IPR002400; GF_cyskn.
DR InterPro; IPR002405; Inh1bin_alpha.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF_beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR00669; INH1BIN.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KM Growth factor.
FT NON_TER 1 1
SQ SEQUENCE 126 AA; 14265 MW; CB824D280F44A394 CRC64;

Query Match 27.3%; Score 44; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 1.1e-32;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 FKELGWDWIIAPLDYEAHCGVCDFPLRSHLEPTNHAIIQTL 112
DB 34 FKELGWDWIIAPLDYEAHCGVCDFPLRSHLEPTNHAIIQTL 77

RESULT 9
09DGN4 PRELIMINARY; PRT; 413 AA.
AC 09DGN4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Growth/differentiation factor 16 precursor protein.
GN Name=gdf16;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20368184; PubMed=10906478; DOI=10.1016/S0925-4773(00)00350-6;
RA Vokes S.A., Krieg P.A.;
RT "gdf16, a novel member of the growth/differentiation factor subgroup
of the TGF-beta superfamily, is expressed in the hindbrain and

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RT epibranchial placodes."
RL Mech. Dev. 95:279-282(2000).
CC -1- SIMILARITY: Belongs to the TGF-beta family.
DR EMBL; AF239676; AAF99597.1; -.
DR HSSP; P08476; INYU.
DR GO; GO:0008083; F: growth factor activity; IEA.
DR GO; GO:0040007; P: growth; IEA.
DR InterPro; IPR002400; GF_cyknok.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001113; TGFb_N.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR Pfam; PF00019; TGF_beta; 1.
DR PRINTS; PR00438; GF_CYS_KNOT.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Signal.
FT SIGNAL 1 23
FT SEQUENCE 413 AA; 46510 MW; 5F1BD7D97E591F6 CRC64;

Query Match 27.3%; Score 44; DB 2; Length 413;
Best Local Similarity 100.0%; Pred. No. 3e-32;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 69 FKEIGMDWITAPLDYEAHCEGVCDPFLRSHLEPTNHAIIOTL 112
Db 321 FKEIGMDWITAPLDYEAHCEGVCDPFLRSHLEPTNHAIIOTL 364

RESULT 10
Q91700 PRELIMINARY; PRT; 79 AA.
ID Q91700
AC Q91700;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Transforming growth factor-beta.
GN Name-activin related;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8335;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Ueno N., Nishimatsu S., Suzuki A., Murakami K.;
RL Submitted (DEC-1989) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the TGF-beta family.
DR EMBL; X17324; CAA35202.1; -.
DR PIR; S21473; S21473.
DR HSSP; P18075; ILXT.
DR GO; GO:0005576; C: extracellular; IEA.
DR GO; GO:0008083; F: growth factor activity; IEA.
DR GO; GO:0008151; P: cell growth and/or maintenance; IEA.
DR Pfam; PF00019; TGF_beta; 1.
DR PRINTS; PR00669; INHIBINA.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor.
SQ SEQUENCE 79 AA; 9036 MW; 7D16A38C8C2A261F CRC64;

Query Match 19.3%; Score 31; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 8.6e-21;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 69 FKEIGMDWITAPLDYEAHCEGVCDPFLRSHLEPTNHAIIOTL 112
Db 49 FKEIGMDWITAPLDYEAHCEGVCDPFLRSHLEPTNHAIIOTL 364

RESULT 11

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Q8K4X4 PRELIMINARY; PRT; 67 AA.
ID Q8K4X4
AC Q8K4X4;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Growth and differentiation factor-6 (Fragment).
GN Name=gdf-6;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Oida S., Morimoto Y., Nakamura T., Terashima T.;
RT "Molecular Cloning of PCR Amplified BMP-Related Genes (GDF-5, 6 and 7)
RT from Rat Tooth Cells Using Modified pBluescript SK+ Vector.";
RL Journal of Hard Tissue Biology 6:16-20(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Oida S., Sena K.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the TGF-beta family.
DR EMBL; AB087405; BAC02714.1; -.
DR HSSP; P08476; INYU.
DR GO; GO:0008083; F: growth factor activity; IEA.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF_beta; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
KW Growth factor.
FT NON_TER 1 1
FT NON_TER 67 67
FT SEQUENCE 67 AA; 7378 MW; F627E22DB1AA268F CRC64;

Query Match 18.0%; Score 29; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 5.3e-19;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 84 YEAYHCEGVCDPFLRSHLEPTNHAIIOTL 112
Db 4 YEAYHCEGVCDPFLRSHLEPTNHAIIOTL 32

RESULT 12
ID GDF6_MOUSE STANDARD; PRT; 125 AA.
AC P43028;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Growth/differentiation factor 6 precursor (GDF-6) (Fragment).
GN Name=gdf6; Synonyms=Gdf-6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Liver;
RX MEDLINE=94195427; PubMed=8145850; DOI=10.1038/366639a0;
RA Storm E.E., Huynh T.V., Copeland N.G., Jenkins N.A., Kingsley D.M.,
RA Lee S.-U.;
RT "Limb alterations in brachypodism mice due to mutations in a new
RT member of the TGF beta-superfamily.";
RL Nature 368:639-643(1994).
CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -1- SIMILARITY: Belongs to the TGF-beta family.
CC -----
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DR EMBL; U08338; AAA18779.1; -.
DR PIR; S43295; S43295.
DR HSSP; P08476; INYU.
DR MGD; MGI:95669; Gdf6.
DR InterPro; IPR002400; GP_cykn0t.
DR InterPro; IPR002405; Inhibin_alpha.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF_beta_1.
DR PRINTS; PR00438; GFCYSKN0T.
DR PRINTS; PR00669; INHIBINA.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
DR Cytokine; Glycoprotein; Growth factor.
FT NON TER 1 1
FT PROPEP <1 5 Potential1.
FT CHAIN 6 125 Growth/differentiation factor 6.
FT DISULFID 24 90 By similarity.
FT DISULFID 53 122 By similarity.
FT DISULFID 57 124 By similarity.
FT DISULFID 89 89 Interchain (By similarity).
SQ SEQUENCE 125 AA; 14373 MW; 10FRA25B7748DA32 CRC64;

Query Match 18.0%; Score 29; DB 1; Length 125;
Best Local Similarity 100.0%; Pred. No. 9e-19;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 84 YEAYHCEGVCDPPLRSHLEPTTHAIQTLL 112
DB 48 YEAYHCEGVCDPPLRSHLEPTTHAIQTLL 76
-----
RESULT 13
Q6P158 PRELIMINARY; PRT; 201 AA.
O6P158
AC Q6P158;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE LOC392255 protein (Fragment).
GN Name=LOC392255;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RX MEDLINE=22388957; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Murusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Paley J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grummond J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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[2]
RN      SEQUENCE FROM N.A..
RP      TISSUE=Testis;
RC      Strauberg R.;
RL      Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
CC      -I SIMILARITY: Belongs to the TGF-beta family.
DR      EMBL; BC043222; AAH43222.1; -.
RS      HSSP; P01137; ITLA.
DN      GO: 0008063; F:growth factor activity; IEA.
DR      InterPro; IPRO02400; GF_cysknoc.
DR      InterPro; IPRO01839; TGfb.
DR      Pfam; PF00019; TGF_beta_1.
DR      PRINTS; PR00438; GFCYSKNOT.
DR      PRODOM; PD000357; TGFB; 1.
DR      SMART; SMO0204; TGFB; 1.
DK      PROSITE; PS00250; TGF_BETA_1; 1.
KW      Growth factor.
FT      NON TER
SQ      SEQUENCE   201 AA;  22441 MW;  FFRIID52EEB0517A CRC64;

Query Match          18.0%; Score 29; DB 2; Length 201;
Best Local Similarity 100.0%; Pred. No. 1,3e+18;
Matches    29; Conservative     0; Mismatches       0; Indels         0; Gaps           0;
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Cy      84 YEAYHCGVCDPLRSLHPNNAIIQTL 112
Db      124 YEAYHCGVCDPLRSHLPENNAIIQLT 152

RESULT 14
GDF6_BOVIN STANDARD; PRI; 436 AA.
ID ID_GDF6_BOVIN STANDARD; PRI; 436 AA.
AC P55106;
DT DT_01-OCT-1996 (Rel. 34, Created)
DT DT_01-OCT-1996 (Rel. 34, Last sequence update)
DT DT_05-JUL-2004 (Rel. 44, Last annotation update)
DE Growth/differentiation factor 6 precursor (GDF-6) (Cartilage-derived morphogenetic protein 2) (CDDP-2) (Fragment).
GN Name=GDF6; Synonyms=CDDP2;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; CC Bovinae; BOB
OK NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Articular cartilage;
RX MEDLINE=95050604; PubMed=7961761;
RA Chang S., Hoang B., Thomas J.T., Vukicevic S., Luyten F.P., RA Ryba N.J.P., Kozak C.A., Reddi A.H., Moos M.; RT "Cartilage-derived morphogenetic proteins. New members of the transforming growth factor-beta superfamily predominantly expressed in long bones during human embryonic development."; RL J. Biol. Chem. 269:28227-28234(1994).
CC -I SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -I SIMILARITY: Belongs to the TGF-beta family.
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Search completed: July 15, 2005, 15:22:25
Job time : 177 secs

DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KM Cysteine; Glycoprotein; Growth factor.
FT NON_TER 1
FT PROPEP 1
FT CHAIN 317 316 Potential.
FT DISULFID 335 436 Growth/differentiation factor 6.
FT DISULFID 364 401 By similarity.
FT DISULFID 368 433 By similarity.
FT DISULFID 400 400 By similarity.
FT CARBOHYD 27 27 Interchain (By similarity).
FT CARBOHYD 89 89 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 89 89 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 436 AA; 47873 MW; B0688R12ER8AE9ID CRC64;

Query Match 18.0%; Score 29; DB 1; Length 436;
Best Local Similarity 100.0%; Pred. No. 2.6e-18;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 YEAYHCEGVCDPPLRSHLEPTNHAIIQTL 112
DB 359 YEAYHCEGVCDPPLRSHLEPTNHAIIQTL 387

RESULT 15

OGHA10 PRELIMINARY; PRT; 452 AA.
AC OGHA10;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Growth differentiation factor 16.
GN Name=gdf16;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RA Guo J.H.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the TGF-beta family.
DR EMBL; AJ537426; CAD60336.2; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR GO; GO:0040007; P:growth; IEA.
DR InterPro; IPR002400; GP_cysknot.
DR InterPro; IPR002405; Inhibin_alpha.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR Pfam; PF00019; TGF_beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR00669; INHIBINA.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KM Growth factor.
SQ SEQUENCE 452 AA; 51013 MW; DF756875E4C1B52A CRC64;

Query Match 18.0%; Score 29; DB 2; Length 452;
Best Local Similarity 100.0%; Pred. No. 2.6e-18;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 YEAYHCEGVCDPPLRSHLEPTNHAIIQTL 112
DB 375 YEAYHCEGVCDPPLRSHLEPTNHAIIQTL 403

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Query Match	100.0%;	Score 161;	DB 2;	Length 161;
Best Local Similarity	100.0%;	Pred. No. 7,7e-145;		
Matches 161;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
Qy	1	AGSRKANIIGRRRRRTALAGTRGAQSGGGGGGGGGGGGGGGGGAGRGHGRGRSRC	60	
Db	1	AGSRKANIIGRRRRRTALAGTRGAQSGGGGGGGGGGGGGGGGGAGRGHGRGRSRC	60	
Qy	61	SRKSLHNDPEKELGQMDWIIAPLDYEAYHNEGICDPDLRSHLEPTNHAIIQTLLNSMAPDA	120	
Db	61	SRKSLHNDPEKELGQMDWIIAPLDYEAYHNEGICDPDLRSHLEPTNHAIIQTLLNSMAPDA	120	
Qy	121	APASCCVPARLSPISILYIDANNVYVKQYEMVVEACCCR	161	
Db	121	APASCCVPARLSPISILYIDANNVYVKQYEMVVEACCCR	161	
RESULT 2				
ABG76038				
ID	ABG76038	standard; protein; 151 AA.		
XX	AC	ABG76038;		
XX	DT	30-APR-2003 (first entry)		
XX	DE	Human GDF-7 C-terminus.		
XX	KM	GDF-5; growth differentiation factor 5; TGF-beta; human;		
XX	KM	transforming growth factor beta; skeletal development; endometriosis;		
XX	KM	cartilage differentiation; cell proliferative disease; uterine tumour;		
XX	KM	bone dysplasia; spondyloepiphyseal dysplasia; achondroplasia;		
XX	KM	dysplasia epiphysealis; metaphyseal dysostosis; hyperchondroplasia;		
XX	KM	enchondromatosis; hypophosphatasia; osteopetrosis; hyperphosphatasia;		
XX	KM	cranioectophraseal dysplasia; osteogenesis imperfecta; transgenic;		
XX	OS	idiopathic osteoporosis; Engelman's disease; GDF-7.		
XX	XX	Homo sapiens.		
XX	PN	US2002165361-A1.		
XX	PD	07-NOV-2002.		
XX	PF	12-JUN-2001; 2001US-00880708.		
XX	PR	12-JAN-1993; 93US-00003144.		
XX	PR	12-JAN-1994; 94WO-US0000657.		
XX	PR	31-MAY-1995; 95US-00455559.		
XX	PR	01-SEP-1998; 98US-00145060.		
XX	PA	(LEES/) LEE S.		
XX	PA	(HUYN/) HUYNH T.		
XX	P1	Lee S, Huynh T;		
XX	DR	WPI, 2003-255226/25.		
XX	PT	New antibody specifically binding to a GDF-5 polypeptide, useful for		
XX	PT	diagnosing and treating cell proliferative disorders with aberrant GDF-5		
XX	PT	activity, such as endometriosis, uterine tumors and those involving		
XX	PT	skeletal tissues.		
XX	PS	Example 2; Fig 3b; 36pp; English.		

Query Match	93.8%;	Score 151;	DB 6;	Length 151;
Best Local Similarity	100.0%;	Prod. No. 2,4e-135;		
Matches 151;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	11	RRRRRTALAGTRGAQSGSGGGGGGGGGGGGGGGGGAGRGHGRGRGRSRSKSLHVDPK	70	
Db	1	RRRRRTALAGTRGAQSGSGGGGGGGGGGGGGGGGGAGRGHGRGRGRSRSKSLHVDPK	60	
Qy	71	ELGWDWDWIIAPLDYEAHCEGVCPEPLRSHEIPTNHAIITQTLNSMAPDAPASCVPAR	130	
Db	61	ELGWDWDWIIAPLDYEAHCEGVCPEPLRSHEIPTNHAIITQTLNSMAPDAPASCVPAR	120	
Qy	131	LSPISTIYIDPANNVVYKQYEDMVEACGCR	161	
Db	121	LSPISTIYIDPANNVVYKQYEDMVEACGCR	151	
RESULT 3				
ID	ADG14199	ADG14199 standard; protein; 151 AA.		
XX	AC	ADG14199;		
XX	DT	26-FEB-2004 (first entry)		
XX	DE	Mouse full length GDF7 protein.		
XX	KW	Mouse; osteogenic protein-1; OP-1; transforming growth factor beta;		
XX	KV	TGFBeta; bone morphogenic protein; BMP5; BMP6; BMP2; BMP4; BMP8/OP2;		
XX	KW	Growth Differentiation Factor; GDF5; GDF6; GDF7; cell growth;		
XX	OS	cell differentiation; cell proliferation.		
XX	XX	Mus musculus.		
XX	PN	US2003185792-A1.		
XX	PD	02-OCT-2003.		
XX	PF	06-JUN-2002; 2002US-00164279.		
XX	PR	22-JAN-1996; 96US-00589552.		
XX	PR	22-JAN-1997; 97US-00786284.		
XX	PR	22-FEB-2001; 2001US-00791946.		
XX	PR	06-JUN-2001; 2001US-0296291P.		
XX	PR	05-FEB-2002; 2002US-0354820P.		
XX	PR	10-APR-2002; 2002US-0371298P.		
XX	PA	(CUR1-) CURIS INC.		
XX	PI	Keck PC, Bosuakonda D;		
XX	DR	WPI; 2004-031977/03.		
XX	PT	Bone morphogenic protein antagonist peptide comprises peptide sequence		
XX	PT	having specified amino acid residues including contiguous amino acids of		
XX	PT	specific amino acid sequences given in the specifications.		

PS Disclosure; SEQ ID NO 61; 88pp; English.

XX The invention relates to a bone morphogenic protein (BMP) antagonist

CC peptide comprising a peptide sequence having 6-50 amino acid residues

CC based on or chosen from the finger 1, heel or finger 2 regions of the

CC TGFbeta (transforming growth factor beta) family proteins osteogenic

CC protein-1 (OP-1), BMP5, BMP6, BMP2, BMP4, BMP8/OP2, GDF5 (Growth

CC Differentiation Factor), GDF6 and GDF7. Also included are a peptide that

CC brings together a cysteine residue on each end and including at least

CC three contiguous amino acids of the protein regions detailed above and a

CC second peptide sequence having a cysteine residue on each end and

CC including at least three contiguous amino acids of 1-34 amino acids of 10

CC different amino acid sequences given in the specifications), a nucleic

CC acid sequence encoding the above peptide, a pharmaceutical preparation

CC comprising a sterile excipient and the above peptide, a peptidomimetic of

CC the peptide and inhibiting or promoting growth, differentiation, or

CC proliferation of a cell by contacting the cell with the above peptide.

CC The antagonist peptides are used to antagonise bone morphogenic protein-

CC like biological activity, preferably osteogenic protein-1 activity. The

CC inventive peptide mimics or enhances the physiological effects of a

CC morphogenic protein, such as osteogenic protein-1 (OP-1). The present

CC sequence is a BMP-like protein used to design the peptides of the

CC invention.

XX

XX Sequence 151 AA:

SO

Query Match 93.8%; Score 151; DB 8; Length 151;

Best Local Similarity 100.0%; Pred. No. 2,4e-135; Mismatches 0; Gaps 0;

Matches 151; Conservative 0; Indels 0; Gaps 0;

QY 11 RRRRTTLAGTGAAGSGGGGGGGGGGGGGGGGGGGGAGRGHGRGRSRCSKSLHYDFK 70

DB 1 RRRRTTLAGTGAAGSGGGGGGGGGGGGGGGGGGGGAGRGHGRGRSRCSKSLHYDFK 60

QY 71 ELGWDWIITAPLDYEAHCEGCDPPLRSHLEPTNHAIIQTLLNSMAPDAPASCVPAR 130

DB 61 ELGWDWIITAPLDYEAHCEGCDPPLRSHLEPTNHAIIQTLLNSMAPDAPASCVPAR 120

QY 131 LSPSITLYIDANNVVKQYEDMVVEACGR 161

DB 121 LSPSITLYIDANNVVKQYEDMVVEACGR 151

RESULT 4

AA051934 standard; protein; 146 AA.

ID AA051934

XX

XX AAM51934;

XX

DT 01-FEB-2002 (first entry)

XX

DE Murine TGFbeta protein superfamily protein GDF7.

XX

KM Mouse; TGFbeta; transforming growth factor beta; mutant; antagonist;

KM agonist; ectopic bone formation; psoriasis; muscular atrophy; scar;

KM formation; fibrosis; cirrhosis; osteopathic; antiproliferative; antifibrotic;

KM hepatocytic; valvular; GDF7.

XX

XX Mus musculus.

OS

XX

OS DE10026713-A1.

PN

XX

PD 06-DEC-2001.

XX

XX 30-MAY-2000; 2000DB-01026713.

PF

XX

PR 30-MAY-2000; 2000DB-01026713.

XX

XX (SEBA/) SEBALD W.

PA

XX

PI Sebal W, Nickel J;

XX

DR WPI; 2002-042559/06.

XX

PT New nuclein of transforming growth factor-beta superfamily protein, useful

PT for treating or preventing e.g. ectopic bone formation, competes for

PT receptor binding.

XX

XX

PS Disclosure; Fig 6; 54pp; German.

XX

CC The present invention relates to murine of a chain of a protein which,

CC when in the form of a homodimer, has antagonistic or partial agonistic

CC activity, and where the mutation results in the protein binding with low

CC affinity to its receptor. The protein is a member of the transforming

CC growth factor beta (TGFbeta) superfamily. The mutant sequences of the

CC invention can be used in the treatment of diseases associated with the

CC overexpression of TGFbeta family proteins, including ectopic bone

CC formation, psoriasis, muscular atrophy, scar formation, fibrosis and

CC cirrhosis. The present sequence is the murine GDF7 protein

CC

XX

XX Sequence 146 AA:

SO

Query Match 90.7%; Score 146; DB 5; Length 146;

Best Local Similarity 100.0%; Pred. No. 1,3e-130; Mismatches 0; Gaps 0;

Matches 146; Conservative 0; Indels 0; Gaps 0;

QY 16 TALAGTGAAGSGGGGGGGGGGGGGGGGGGGGAGRGHGRGRSRCSKSLHYDFKELGMD 75

DB 1 TALAGTGAAGSGGGGGGGGGGGGGGGGGGGGAGRGHGRGRSRCSKSLHYDFKELGMD 60

QY 76 DWIITAPLDYEAHCEGCDPPLRSHLEPTNHAIIQTLLNSMAPDAPASCVPARLSPIS 135

DB 61 DWIITAPLDYEAHCEGCDPPLRSHLEPTNHAIIQTLLNSMAPDAPASCVPARLSPIS 120

QY 136 ILYIDANNVVKQYEDMVVEACGR 161

DB 121 ILYIDANNVVKQYEDMVVEACGR 146

RESULT 5

AA052582 standard; peptide; 102 AA.

ID AA052582

XX

XX AAY92582;

XX

DT 10-AUG-2000 (first entry)

XX

XX

DE GDF-7 finger-1-heel-finger-2 sequence.

XX

KM finger domain; heel region; BMP; TGF-beta family; protein refolding;

KM fusion protein; osteopathic; antibacterial; cytostatic.

XX

XX Mus musculus.

OS

XX

XX Key

XX

XX Domain

XX

XX Location/Qualifiers

XX

XX 2..29

XX /label= finger_1

XX

XX 35..65

XX /label= heel

XX

XX 68..98

XX /label= finger_2

XX

XX WO200020449-A2.

PN

XX

XX 13-APR-2000.

PD

XX

XX 07-OCT-1999; 99WO-US023372.

PF

XX

XX 07-OCT-1998; 98US-0103418P.

PR

XX

PR 16-AUG-1999; 99US-00375333.

XX

XX (STYC) STRYKER CORP.

PA

XX

PI Oppermann H, Tai M, McCartney J;

XX

DR WPI; 2000-303743/26.
XX
XX A biologically active TGF-beta family member fusion protein competent to
PT refold, comprising a C-terminal linked TGF-beta family protein.
PT
XX
PS Disclosure; Page 160; 160pp; English.
XX
CC AAY92554-82 show the finger 1, heel and finger 2 domains of TGF-beta
CC superfamily members. These sequences can be used to form novel fusion
CC proteins. Novel proteins comprise biologically active TGF-beta family
CC member fusion proteins competent to refold under suitable refolding
CC conditions. The fusion proteins comprise: (1) a TGF-beta family protein C
CC-terminal seven cysteine domain, comprising finger 1, finger 2 and heel
CC subdomains; and (2) a heterologous leader sequence domain operatively
CC linked to the C-terminal domain. Truncations, heterodimers and mutants of
CC these fusion proteins and methods of purifying the heterodimers are also
CC claimed. The TGF-beta family proteins can be used to induce the full
CC cascade of morphogenic events which culminate in skeletal tissue
CC formation, including cartilage and endochondral bone formation. They are
CC useful in the binding of fibrin and fibronectin to the implanted matrix,
CC chondroblasts, cartilage formation, vascular invasion, bone formation,
CC remodeling, and bone marrow differentiation. The proteins have improved
CC physical properties such as solubility and stability, improved biological
CC activity, including altered receptor binding and improved targeting
CC capabilities
XX
SQ Sequence 102 AA;
XX
Query Match 63.4%; Score 102; DB 3; Length 102;
Best Local Similarity 100.0%; Pred. No. 6.8e-99;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 60 CSRSKSLHVPKELGMDWIIAPLDYEAHYHCEGCDPFLRSHLEPTNHAIIQTLSNAPD 119
DB 1 CSRSKSLHVPKELGMDWIIAPLDYEAHYHCEGCDPFLRSHLEPTNHAIIQTLSNAPD 60
QY 120 AAPASCCVPARLSPISILYIDAANNVYKQYEDMVVEACGCR 161
DB 61 AAPASCCVPARLSPISILYIDAANNVYKQYEDMVVEACGCR 102
XX
RESULT 6
AAB09557
ID AAB09557 standard; protein; 102 AA.
XX
AC AAB09557;
XX
DT 11-SEP-2000 (first entry)
XX
DE Murine GDF-7, SEQ ID NO:87.
XX
KM TGF-beta superfamily; transforming growth factor-beta;
KM developmental regulation; finger 2 subdomain; basic region;
KM protein refolding; stability; solubility; osteogenic protein; OP;
KM bone morphogenetic protein; BMP; growth/differentiation factor; GDF;
KM inhibin; tissue morphogenesis; regeneration; bone; dental tissue;
KM connective tissue; cartilage; vulnary.
XX
XX Mus musculus.
OS
XX
XX MO200020607-A2.
PN
XX
PD 13-APR-2000.
XX
PF 07-OCT-1999; 99W0-US023371.
XX
PR 07-OCT-1998; 98US-0103418P.
XX
PR 16-AUG-1999; 99US-00374958.
XX
XX (STYC) STRYKER CORP.
PA
XX
XX Oppermann H, Tai M, McCartney J;
PI

XX
XX WPI; 2000-303787/26.
XX
XX Transforming growth factor-beta superfamily member mutant induces tissue
PT morphogenesis in e.g. bone, non-mineralized skeletal tissue, dental
PT tissue and connective tissue and comprises a substitution in a region of
PT the finger 2 domain.
XX
XX
PS Disclosure; Page 161-162; 162pp; English.
XX
XX
CC The invention relates to mutant TGF-beta (transforming growth factor-
CC beta) superfamily members. These mutants comprise one or more amino acid
CC substitutions in the base region of the finger 2 subdomain, and a C-
CC-terminal residue selected from Arg, Ile, Leu, Ser and Ala. In the finger
CC 2 subdomain, basic residues (e.g., Arg, Lys), or residues containing an
CC amide group (e.g., Gln, Asn), are substituted with acidic residues (e.g.,
CC Glu, Asp) or residues containing a hydroxyl group (e.g., Ser, Thr). TGF-
CC-beta superfamily proteins regulate developmental processes and include
CC proteins such as the osteogenic proteins (OPs), bone morphogenetic
CC proteins (BMPs), growth/differentiation factors (GDFs) and inhibins.
CC Specific examples of TGF-beta superfamily mutants encompassed by the
CC invention are the finger 2 subdomain mutants of human osteogenic protein-
CC 1 (OP-1) (AAB09576-B09615). Mutant TGF-beta proteins are used for
CC inducing tissue morphogenesis in bone, non-mineralized skeletal tissue,
CC dental tissue, connective tissue, brain, liver and nerve tissue. The
CC proteins can be used in conjunction with a biocompatible matrix e.g.,
CC collagen, hydroxyapatite or carboxymethylcellulose for regenerating bone,
CC cartilage and/or other mineralized skeletal or connective tissues e.g.,
CC ligament, tendon, muscle, fibrocartilage, joint capsule and
CC intervertebral discs. The OP-1 mutants can be used to repair diseased or
CC damaged mammalian tissue and to prevent or substantially inhibit
CC immune/inflammatory response-mediated tissue damage and scar tissue
CC formation following an injury. Compared to the wild-type TGF-beta
CC superfamily members, the mutant proteins have improved in vitro refolding
CC properties in a pH range of 6-9, increased solubility in aqueous solution
CC and improved stability and/or activity. Sequences AAB09519-B09542 and
CC AAB09553-B09558 represent a variety of wild-type TGF-beta superfamily
CC proteins referred to in the specification
XX
SQ Sequence 102 AA;
XX
Query Match 63.4%; Score 102; DB 3; Length 102;
Best Local Similarity 100.0%; Pred. No. 6.8e-89;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 60 CSRSKSLHVPKELGMDWIIAPLDYEAHYHCEGCDPFLRSHLEPTNHAIIQTLSNAPD 119
DB 1 CSRSKSLHVPKELGMDWIIAPLDYEAHYHCEGCDPFLRSHLEPTNHAIIQTLSNAPD 60
QY 120 AAPASCCVPARLSPISILYIDAANNVYKQYEDMVVEACGCR 161
DB 61 AAPASCCVPARLSPISILYIDAANNVYKQYEDMVVEACGCR 102
XX
RESULT 7
AAB02823
ID AAB02823 standard; protein; 102 AA.
XX
XX AAB02823;
XX
XX 22-AUG-2000 (first entry)
XX
DE Mouse GDF-7 amino acid sequence SEQ ID NO:87.
XX
XX
KM Tumour growth factor beta; TGF-beta; morphogenic protein; BMP; OP;
KM bone morphogenic protein; osteogenic protein; mutant; modified;
KM finger 2 sub-domain; finger 1 domain; heel domain; chimeric protein;
KM osteogenic; proliferative; antiinflammatory; tissue morphogenesis;
KM tissue repair; regeneration; proliferation; differentiation.
XX
XX Mus musculus.
OS
XX
XX MO200020591-A2.
PN

PD 13-APR-2000.
 XX
 PF 07-OCT-1999; 99WO-US023370.
 XX
 PR 07-OCT-1998; 98US-0103418P.
 PR 16-AUG-1999; 99US-00374936.
 XX
 PA (STRYK) STRYKER CORP.
 XX
 PI Oppermann H, Tai M, McCartney J;
 DR WPI; 2000-303776/26.
 XX
 PT Novel TGF-beta superfamily mutant chimeric protein, useful for inducing
 PT tissue morphogenesis in e.g. bone, comprises a dimer consisting of one
 PT monomer containing domains from two family members.
 XX
 PS Disclosure; Page 148; 149pp; English.
 XX
 CC The present invention describes a tumour growth factor beta (TGF-beta)
 CC superfamily chimeric protein (I) derived from at least 2 different
 CC members of the superfamily comprising a dimer with one monomer that
 CC contains a finger 2 domain derived from a first family member and a
 CC finger 1 domain and heel domain, both derived from a second family
 CC member. The monomer further comprises a conserved C-terminal cysteine
 CC skeleton. (I) has osteogenic, proliferative and antiinflammatory
 CC activities. The TGF-beta superfamily chimeric proteins (I) are useful for
 CC inducing tissue morphogenesis (i.e. molecules capable of tissue repair
 CC and regeneration and/or inhibiting inflammation) in bone, non-mineralised
 CC skeletal tissue, dental tissue, connective tissue, brain, liver and nerve
 CC and for inducing the proliferation and differentiation of uncommitted
 CC progenitor cells in a tissue-specific manner to support new tissue
 CC formation. AA929887 to AA929897 and AA802748 to AA802824 represent
 CC sequences used in the exemplification of the present invention
 CC
 SQ Sequence 102, AA;
 XX
 Query Match 63.4%; Score 102; DB 3; Length 102;
 Best Local Similarity 100.0%; Pred. No. 6.8e-69;
 Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 60 CSRKSLHVDPEKELGMDWIIAPLDYEAHYHCEGVCDPFLRSHLEPTNHAIIQTLLNSMAPD 119
 DB 1 CSRKSLHVDPEKELGMDWIIAPLDYEAHYHCEGVCDPFLRSHLEPTNHAIIQTLLNSMAPD 60
 QY 120 AAPASCCVPARLSPISILYIDANNVVKQYEDMVVEACGCR 161
 DB 61 AAPASCCVPARLSPISILYIDANNVVKQYEDMVVEACGCR 102
 RESULT 8
 AAR78738 AAR78738 standard; protein; 240 AA.
 XX
 AC AAR78738;
 XX
 DT 25-MAR-2003 (revised)
 DT 23-NOV-1995 (first entry)
 XX
 DE Murine mV1 protein.
 XX
 KM Bone morphogenetic protein; mV1; tendon; ligament.
 XX
 OS Mus musculub.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 7 /label= V,A,E,G
 FT Misc-difference 8 /label= S,P,T,A
 FT Misc-difference 15 /label= S,R
 FT

FT Misc-difference 16 /label= L,P,Q,R
 FT Misc-difference 26 /label= C,W
 FT Misc-difference 37 /label= V,A,D,G
 FT Misc-difference 103 /label= V,A,E,G
 FT Misc-difference 104 /label= Q,K,E
 XX
 XX WO9516035-A2.
 XX
 PN 15-JUN-1995.
 PD
 XX
 XX 06-DEC-1994; 94WO-US014030.
 PF
 XX 07-DEC-1993; 93US-00164103.
 PR 25-MAR-1994; 94US-00217780.
 PR 02-NOV-1994; 94US-00333576.
 XX
 PA (GENY) GENETICS INST. INC.
 PA (HARD) HARVARD COLLEGE.
 PI Celeste AJ, Wozney JM, Rosen VA, Wolfman NM, Thomsen GH;
 PI Melton DA;
 DR WPI; 1995-224320/29.
 DR N-PSDB; AA096223.
 XX
 PT Bone morphogenetic proteins -12 and -13 and corresp. DNA - used in
 PT compar. for inducing tendon/ligament-like tissue formation.
 XX
 PS Example; Page 68-70; 84pp; English.
 XX
 CC Oligos #6 and #7 (AA096223 & AA096219) are used as primers for the
 CC amplification of a 275 bp DNA probe, the internal 269 bp of which
 CC corresp. to nts #607 to #865 of AA096207, from the BMP-12 encoding
 CC plasmid subclone PCR1-1#2. This probe was radioactively labelled and used
 CC to screen a murine genomic library. DNA sequence analysis of one of
 CC positively hybridizing recombinants named MVR3 indicates that it encodes
 CC a portion of the mouse gene corresp. to the PCR product mV1 (murine
 CC homolog of the human BMP-12 sequence AA096207. The partial DNA sequence
 CC of this subclone and corresp. AA translation are given in AA096223 &
 CC AAR78738. (Updated on 25-MAR-2003 to correct PN field.)
 CC
 SQ Sequence 240 AA;
 XX
 Query Match 62.1%; Score 100; DB 2; Length 240;
 Best Local Similarity 100.0%; Pred. No. 1.1e-86;
 Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 62 RKSILHVDPEKELGMDWIIAPLDYEAHYHCEGVCDPFLRSHLEPTNHAIIQTLLNSMAPDAA 121
 DB 141 RKSILHVDPEKELGMDWIIAPLDYEAHYHCEGVCDPFLRSHLEPTNHAIIQTLLNSMAPDAA 200
 QY 122 PASCVPARLSPISILYIDANNVVKQYEDMVVEACGCR 161
 DB 201 PASCVPARLSPISILYIDANNVVKQYEDMVVEACGCR 240
 RESULT 9
 AAM26594 AAM26594 standard; protein; 240 AA.
 XX
 AC AAM26594;
 XX
 DT 25-MAR-2003 (revised)
 DT 21-JUN-1998 (first entry)
 XX
 DE Murine BMP-12 homologue fragment.
 XX
 KM BMP-12; bone morphogenetic protein; mouse; tendon; ligament;
 XX

KW	wound healing; tissue repair; carpal tunnel syndrome; tendonitis;
XX	therapy.
XX	Mus musculus.
OS	
XX	Key Location/Qualifiers
FH	7
FT	/label= Val, Ala, Glu, Gly
FT	/note= "encoded by GNG"
FT	Misc-difference 8
FT	/label= Ser, Pro, Thr, Ala
FT	/note= "encoded by NCG"
FT	15
FT	Misc-difference 15
FT	/label= Ser, Arg
FT	/note= "encoded by AGN"
FT	16
FT	/label= Leu, Pro, Gln, Arg
FT	/note= "encoded by CNG"
FT	26
FT	Misc-difference 26
FT	/label= Cys, Trp
FT	/note= "encoded by TGN"
FT	37
FT	/label= Val, Ala, Asp, Gly
FT	/note= "encoded by GNC"
FT	103
FT	Misc-difference 103
FT	/label= Val, Ala, Glu, Gly
FT	/note= "encoded by GNG"
FT	104
FT	/label= Lys, Gln
FT	/note= "encoded by NMG"
XX	
PN	US6568882-A.
XX	
XX	19-AUG-1997.
PD	
XX	
PP	22-DEC-1994; 94US-00362670.
XX	
PR	07-DEC-1993; 93US-00164103.
PR	25-MAR-1994; 94US-00217780.
PR	02-NOV-1994; 94US-00333576.
XX	
XX	(HARD) HARVARD COLLEGE.
PA	(GENY) GENETICS INST INC.
XX	
PI	Melton DA, Thomsen GH, Wozney JM, Wolfman NM, Rosen VA;
PI	Celeste AJ;
XX	
DR	WPI: 1997-424370/39.
DR	N-PSDB; AAT90396.
XX	
XX	Inducing tendon and ligament formation using BMP-12, BMP-13 or MP-52 -
PT	useful for tissue healing and repair, treatment of tendonitis, improving
PT	fixation of tendons to bone etc.
XX	
PS	Example 1, Col 65-68; 43pp; English.
XX	
CC	This polypeptide comprises a fragment of a murine homologue of human bone
CC	morphogenetic protein 12 (BMP-12) (see also AAW26589). Its amino acid
CC	sequence was deduced from DNA subclone mVI (see AAT90396), isolated from
CC	murine genomic DNA using primers (see AAT90393-94) based on human BMP-12
CC	sequences. Human BMP-12, BMP-13 (see AAW26591) and MP52 (see AAW26590)
CC	polypeptides are used in a claimed method for inducing tendon and
CC	ligament formation. (Updated on 25-MAR-2003 to correct PF field.)
XX	
SO	Sequence 240 AA:
QY	Query Match 62.1%; Score 100; DB 2; Length 240;
	Best Local Similarity 100.0%; Pred. No. 1.le-86;
DB	Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	62 RSLIIVDFEELGMDMIITAPLDYEAVHGCVCDPFLRSHLEPTNHAIITQLINSMAPPAA 121
	141 RSLIHVDPEELGMDMIITAPLDYEAVHGCVCDPFLRSHLEPTNHAIITQLINSMAPPAA 200

Q#	122	PASCCVPARLSPISILYTDANNVYKQYEDWVACGCR	161
Db	201	PASCCVPARLSPISILYTDANNVYKQYEDWVACGCR	240
RESULT	10		
ID	AAE10984		
XX	AAE10984	standard; protein; 240 AA.	
AC	AAE10984;		
XX			
DT	18-DEC-2001	(first entry)	
XX			
DE	Murine partial mV1 protein.		
XX			
KW	Mouse; bone morphogenic protein; BMP-12; vulnerary; antiinflammatory;		
KW	analgesic; gene therapy; transforming growth factor-beta; TGF-beta;		
KW	tissue formation; wound healing; tissue repair; ligament defect;		
KW	carpal tunnel syndrome; tendonitis; mV1.		
XX			
OS	Mus sp.		
XX			
FH	Key	Location/Qualifiers	
FT	Misc-difference	7	
FT		/label= Unknown	
FT		/note= "Encoded by GNG"	
FT		8	
FT	Misc-difference	/label= Unknown	
FT		/note= "Encoded by NCG"	
FT		15	
FT	Misc-difference	/label= Unknown	
FT		/note= "Encoded by AGN"	
FT		16	
FT	Misc-difference	/label= Unknown	
FT		/note= "Encoded by CNG"	
FT		26	
FT	Misc-difference	/label= Unknown	
FT		/note= "Encoded by TGN"	
FT		37	
FT	Misc-difference	/label= Unknown	
FT		/note= "Encoded by GNC"	
FT		103	
FT	Misc-difference	/label= Unknown	
FT		/note= "Encoded by GNG"	
FT		104	
FT	Misc-difference	/label= Unknown	
FT		/note= "Encoded by NAG"	
XX			
PN	US6284872-B1.		
XX			
PD	04-SEP-2001.		
XX			
PF	28-FEB-1997;	97US-00808324.	
XX			
PR	07-DEC-1993;	93US-00164103.	
PR	25-MAR-1994;	94US-00217780.	
PR	02-NOV-1994;	94US-00333576.	
PR	22-DEC-1994;	94US-00362670.	
XX			
PA	(GENY) GENETICS INST INC.		
PA	(HARD) HARVARD COLLEGE.		
XX			
PI	Celeste AU; Wozney JM; Rosen VA; Wolfman NM; Thomsen GH;		
XX			
PI	Melton DA;		
XX			
DR	WPI; 2001-588978/66.		
XX			
DR	N-PSDB; AAD18335.		
XX			
PT	New chimeric DNAs, useful for treating tendonitis, carpal tunnel syndrome		
PT	and other tendon and ligament defects, comprises DNA encoding propeptide		
PT	linked to DNA encoding bone morphogenetic proteins (BMP)-12, BMP-13 or		
PT	BMP2.		

XX Example 1; Col 67-70; 42pp; English.

PS The invention relates to a chimeric DNA comprising a DNA sequence

CC encoding a propeptide from a member of the transforming growth factor

CC (TGF)-beta superfamily of proteins. This DNA is linked to a DNA sequence

CC encoding an amino acid sequence encoding a mature polypeptide consisting

CC of Bone Morphogenetic Protein (BMP)-12, BMP-13 or MP52 protein. The DNA

CC sequences are useful for producing proteins which induce tendon/ligament

CC like tissue formation, and for isolating proteins with similar activity. The

CC sequences encoding BMP-12 related proteins with similar activity. The

CC proteins are useful for the induction of tendon/ligament-like tissue

CC formation, wound healing, ligament and other tissue repair, augmenting

CC the activity of bone morphogenetic proteins, and for treating tendinitis,

CC carpal tunnel syndrome and other tendon and ligament defects. The present

CC sequence is murine partial mvl protein which is homologous to human BMP-

CC 12 or VL-1 sequences of the invention

XX

XX Sequence 240 AA;

SQ

Query Match 62.1%; Score 100; DB 4; Length 240;

Best Local Similarity 100.0%; Pred. No. 1.1e-86;

Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 RKSLHVDPEKLGMDWIIAPLDYEAHCEGCDPPLRSHLEPTNHAIIQTLLNSMAPDAA 121

DB 141 RKSLHVDPEKLGMDWIIAPLDYEAHCEGCDPPLRSHLEPTNHAIIQTLLNSMAPDAA 200

QY 122 PASCVPARLSPISILYIDAANNVVKQYEDMVVEACGCR 161

DB 201 PASCVPARLSPISILYIDAANNVVKQYEDMVVEACGCR 240

RESULT 11

ABG73300

ID ABG73300 standard; protein; 240 AA.

XX

XX ABG73300;

AC

XX

DT 30-APR-2003 (first entry)

DE

XX

XX Amino acid sequence for murine mvl protein.

XX

XX Mouse; bone morphogenetic protein-12; BMP-12; BMP-12 related protein;

KM BMP-13; VL-1; BMP/TGF-beta/Vg-1 family; tissue repair; tendinitis;

KM tendon/ligament-like tissue formation; trauma induced tendon defect;

KM tendon/ligament-like tissue healing; tendon damage; ligament damage;

KM tendon fixation; ligament fixation; congenital; ligament defect;

KM cosmetic plastic surgery; vulnerability; murine; mvl.

XX

OS Mus sp.

XX

XX Key

XX Location/Qualifiers

FT Misc-difference 7

FT /label= Val, Ala, Glu, Gly

FT /note= "Encoded by GNG"

FT Misc-difference 8

FT /label= Ser, Pro, Thr, Ala

FT /note= "Encoded by NCG"

FT Misc-difference 15

FT /label= Ser, Arg

FT /note= "Encoded by AGN"

FT Misc-difference 16

FT /label= Leu, Pro, Gln, Arg

FT /note= "Encoded by CNG"

FT Misc-difference 26

FT /label= Cys, Trp

FT /note= "Encoded by TGN"

FT Misc-difference 37

FT /label= Val, Ala, Asp, Gly

FT /note= "Encoded by GNC"

FT Misc-difference 103

FT /label= Val, Ala, Glu, Gly

FT /note= "Encoded by GNG"

FT Misc-difference 104

FT /label= Gln, Lys, Glu

FT /note= "Encoded by NAG"

XX

XX US2002160494-A1.

XX

XX 31-OCT-2002.

XX

XX 31-AUG-2001; 2001US-00945182.

XX

XX 07-DEC-1993; 93US-00164103.

XX 25-MAR-1994; 94US-00217780.

XX 02-NOV-1994; 94US-0033576.

XX 22-DEC-1994; 94US-00362670.

XX 28-FEB-1997; 97US-00808324.

XX

XX (CELE/) CELESTE A J.

XX (WOZN/) WOZNEY J M.

XX (ROSE/) ROSEN V A.

XX (WOLF/) WOLFMAN N M.

XX (THOM/) THOMSEN G H.

XX (MELT/) MELTON D A.

XX

XX Celeste AJ, Wozney JM, Rosen VA, Wolfman NM, Thomsen GH,

XX Melton DA;

XX

XX WPI; 2003-238228/23.

XX N-PSDB; ABX11157.

XX

XX New bone morphogenetic proteins (designated BMP-12) or related proteins,

XX useful for inducing tendon/ligament-like tissue formation in a patient,

XX or for tendon/ligament-like tissue healing or repair (e.g. for treating

XX tendinitis).

XX

XX Example 1; Page 37; 46pp; English.

XX

XX The present invention relates to the isolation of human bone

XX morphogenetic protein-12 (BMP-12) protein and a BMP-12 related protein

XX (designated BMP-13 or VL-1), and the polynucleotide sequences encoding

XX them. The novel BMPs are members of the BMP/TGF-beta/Vg-1 family of

XX proteins. BMP-12 and VL-1 are characterised by their ability to induce

XX the formation of tendon/ligament-like tissue. The BMP-12 proteins of the

XX invention are useful for inducing tendon/ligament-like tissue formation

XX in a patient. They are particularly useful for tendon/ligament-like

XX tissue healing and tissue repair, e.g. for treating tendinitis, or other

XX tendon or ligament defects in a patient. The polynucleotide sequences

XX encoding the BMP-12 proteins are useful for inducing tendon/ligament-like

XX tissue formation in a patient, and for tendon/ligament-like tissue

XX healing and tissue repair. The BMP-12 polypeptide and polynucleotide

XX sequences may be used for preventing damage to tendon or ligament tissue,

XX to improve fixation of tendon or ligament to bone or other tissues, to

XX repair congenital or trauma induced tendon or ligament defects, and in

XX cosmetic plastic surgery for attachment or repair of tendons or

XX ligaments. The present sequence represents murine mvl protein, a

XX homologue of human BMP-12/VL-1

XX

SQ

SQ Sequence 240 AA;

Query Match 62.1%; Score 100; DB 6; Length 240;

Best Local Similarity 100.0%; Pred. No. 1.1e-86;

Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 RKSLHVDPEKLGMDWIIAPLDYEAHCEGCDPPLRSHLEPTNHAIIQTLLNSMAPDAA 121

DB 141 RKSLHVDPEKLGMDWIIAPLDYEAHCEGCDPPLRSHLEPTNHAIIQTLLNSMAPDAA 200

QY 122 PASCVPARLSPISILYIDAANNVVKQYEDMVVEACGCR 161

DB 201 PASCVPARLSPISILYIDAANNVVKQYEDMVVEACGCR 240

RESULT 12

AAE10977
 ID AAE10977 standard; protein; 72 AA.
 AC AAE10977;
 DT 18-DEC-2001 (first entry)
 DE Murine clone mV1 protein.
 XX
 XX Mouse; bone morphogenic protein; BMP-12; vulnery; antiinflammatory;
 KW analgesic; gene therapy; transforming growth factor-beta; TGF-beta;
 KW tissue formation; wound healing; tissue repair; ligament defect;
 KW carpal tunnel syndrome; tendonitis; mV1.
 OS Mus sp.
 XX
 XX US6284872-B1.
 PN 04-SEP-2001.
 PD 28-FEB-1997; 97US-00808324.
 PF 07-DEC-1993; 93US-00164103.
 PR 25-MAR-1994; 94US-00217780.
 PR 02-NOV-1994; 94US-00333576.
 PR 22-DEC-1994; 94US-00362670.
 PA (GEMV) GENETICS INST INC.
 PA (HARD) HARVARD COLLEGE.
 PI Celeste AJ, Wozney JM, Rosen VA, Wolfman NM, Thomsen GH;
 PI Melton DA;
 XX
 XX WPI; 2001-588978/66.
 DR N-PSDB; AAD18321.
 DR
 PT New chimeric DNAs, useful for treating tendonitis, carpal tunnel syndrome
 PT and other tendon and ligament defects, comprises DNA encoding propeptide
 PT linked to DNA encoding bone morphogenetic proteins (BMP-12, BMP-13 or
 PT MP52.
 PT
 XX
 XX Example 1; Col 47-48; 42pp; English.
 XX
 CC The invention relates to a chimeric DNA comprising a DNA sequence
 CC encoding a propeptide from a member of the transforming growth factor
 CC (TGF)-beta superfamily of proteins. This DNA is linked to a DNA sequence
 CC encoding an amino acid sequence encoding a mature polypeptide consisting
 CC of Bone Morphogenetic Protein (BMP)-12, BMP-13 or MP52 protein. The DNA
 CC sequences are useful for producing proteins which induce tendon/ligament
 CC like tissue formation, and for isolating and cloning further DNA
 CC sequences encoding BMP-12 related proteins with similar activity. The
 CC proteins are useful for the induction of tendon/ligament-like tissue
 CC formation, wound healing, ligament and other tissue repair, augmenting
 CC the activity of bone morphogenetic proteins, and for treating tendonitis,
 CC carpal tunnel syndrome and other tendon and ligament defects. The present
 CC sequence is murine clone, mV1 protein which is homologous to human BMP-12
 CC or VL-1 sequences of the invention
 CC
 XX
 XX Sequence 72 AA:
 SQ
 Query Match 44.7%; Score 72; DB 4; Length 72;
 Best Local Similarity 100.0%; Pred. No. 1.7e-60;
 Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 77 WIIAPLDYEAHYHCEGCDPFLRSHLEPTNNAIIQTLLNSAAPAPASCCVPARLSPISI 136
 DB 1 WIIAPLDYEAHYHCEGCDPFLRSHLEPTNNAIIQTLLNSAAPAPASCCVPARLSPISI 60
 QY 137 LYTDAANNVYK 148
 DB 61 LYTDAANNVYK 72

RESULT 13
 ABG73293
 ID ABG73293 standard; protein; 72 AA.
 AC ABG73293;
 DT 30-APR-2003 (first entry)
 DE Homologue of human BMP-12/VL-1 encoded by DNA from murine clone mV1.
 XX
 XX Mouse; bone morphogenetic protein-12; BMP-12; BMP-12 related protein;
 KW BMP-13; VL-1; BMP/TGF-beta/Vg-1 family; tissue repair; tendonitis;
 KW tendon/ligament-like tissue formation; trauma induced; tendon defect;
 KW tendon/ligament-like tissue healing; tendon damage; ligament damage;
 KW tendon fixation; ligament fixation; congenital; ligament defect;
 KW cosmetic plastic surgery; vulnery; murine; mV1.
 OS Mus sp.
 XX
 XX US2002160494-A1.
 PN 31-OCT-2002.
 PD 31-AUG-2001; 2001US-00945182.
 PF 07-DEC-1993; 93US-00164103.
 PR 25-MAR-1994; 94US-00217780.
 PR 02-NOV-1994; 94US-00333576.
 PR 22-DEC-1994; 94US-00362670.
 PR 28-FEB-1997; 97US-00808324.
 PA (CELESTE) CELESTE A J.
 PA (WOZNEY) WOZNEY J M.
 PA (ROSEN) ROSEN V A.
 PA (WOLF) WOLFMAN N M.
 PA (THOM) THOMSEN G H.
 PA (MELT) MELTON D A.
 PI Celeste AJ, Wozney JM, Rosen VA, Wolfman NM, Thomsen GH;
 PI Melton DA;
 XX
 XX WPI; 2003-238228/23.
 DR N-PSDB; ABX11145.
 DR
 PT New bone morphogenetic proteins (designated BMP-12) or related proteins,
 PT useful for inducing tendon/ligament-like tissue formation in a patient,
 PT or for tendon/ligament-like tissue healing or repair (e.g. for treating
 PT tendonitis).
 PT
 XX
 XX Example 1; Page 25-26; 46pp; English.
 XX
 CC The present invention relates to the isolation of human bone
 CC morphogenetic protein-12 (BMP-12) protein and a BMP-12 related protein
 CC (designated BMP-13 or VL-1), and the polynucleotide sequences encoding
 CC them. The novel BMPs are members of the BMP/TGF-beta/Vg-1 family of
 CC proteins. BMP-12 and VL-1 are characterised by their ability to induce
 CC the formation of tendon/ligament-like tissue. The BMP-12 proteins of the
 CC invention are useful for inducing tendon/ligament-like tissue formation
 CC in a patient. They are particularly useful for tendon/ligament-like
 CC tissue healing and tissue repair, e.g. for treating tendonitis, or other
 CC tendon or ligament defects in a patient. The polynucleotide sequences
 CC encoding the BMP-12 proteins are useful for inducing tendon/ligament-like
 CC tissue formation in a patient, and for tendon/ligament-like tissue
 CC healing and tissue repair. The BMP-12 polypeptide and polynucleotide
 CC sequences may be used for preventing damage to tendon or ligament tissue,
 CC to improve fixation of tendon or ligament to bone or other tissues, to
 CC repair congenital or trauma induced tendon or ligament defects, and in
 CC cosmetic plastic surgery for attachment or repair of tendons or
 CC ligaments. The present sequence represents a homologue of human BMP-12/VL-
 CC -1 encoded by DNA from murine clone mV1
 CC
 XX
 XX Sequence 72 AA:
 SQ

Query Match 44.7%; Score 72; DB 6; Length 72;
 Best Local Similarity 100.0%; Pred. No. 1,7e-60;
 Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 137 LYIDANNVYK 148
 61 LYIDANNVYK 72

RESULT 14
 AAB09558
 ID AAB09558 standard; protein, 102 AA.

AC AAB09558;
 XX
 XX 11-SEP-2000 (first entry)
 DT
 XX Human CDMF-3, SEQ ID NO:88.
 DE
 XX TGF-beta superfamily; transforming growth factor-beta;
 KW developmental regulation; finger 2 subdomain; basic region;
 KW protein refolding; stability; solubility; osteogenic protein; OP;
 KW bone morphogenetic protein; BMP; growth/differentiation factor; GDF;
 KW inhibin; tissue morphogenesis; regeneration; bone; dental tissue;
 KW connective tissue; cartilage; vulvectomy.
 XX
 OS Homo sapiens.
 XX
 PN W0200020607-A2.
 PD 13-APR-2000.
 PF 07-OCT-1999; 99WO-US023371.
 XX
 PR 07-OCT-1998; 98US-0103418P.
 PR 16-AUG-1999; 99US-00374958.
 XX
 PA (STYC) STRYKER CORP.
 XX
 PI Oppermann H, Tai M, McCartney J;
 DR WPI; 2000-303787/26.

PT Transforming growth factor-beta superfamily member mutant induces tissue
 PT morphogenesis in e.g. bone, non-mineralized skeletal tissue, dental
 PT tissue and connective tissue and comprises a substitution in a region of
 PT the finger 2 domain.
 XX
 PS Disclosure; Page 162; 162pp; English.

CC The invention relates to mutant TGF-beta (transforming growth factor-
 CC beta) superfamily members. These mutants comprise one or more amino acid
 CC substitutions in the base region of the finger 2 subdomain, and a C-
 CC terminal residue selected from Arg, Ile, Leu, Ser and Ala. In the finger
 CC 2 subdomain, basic residues (e.g., Arg, Lys), or residues containing an
 CC amide group (e.g., Gln, Asn), are substituted with acidic residues (e.g.,
 CC Glu, Asp) or residues containing a hydroxyl group (e.g., Ser, Thr). TGF-
 CC beta superfamily proteins regulate developmental processes and include
 CC proteins such as the osteogenic proteins (OPs), bone morphogenetic
 CC proteins (BMPs), growth/differentiation factors (GDFs) and inhibins.
 CC Specific examples of TGF-beta superfamily mutants encompassed by the
 CC invention are the finger 2 subdomain mutants of human osteogenic protein-
 CC 1 (OP-1) (AAB09576-B09615). Mutant TGF-beta proteins are used for
 CC inducing tissue morphogenesis in bone, non-mineralized skeletal tissue,
 CC dental tissue, connective tissue, brain, liver and nerve tissue. The
 CC proteins can be used in conjunction with a biocompatible matrix e.g.,
 CC collagen, hydroxyapatite or carboxymethylcellulose for regenerating bone,
 CC cartilage and/or other mineralized skeletal or connective tissues e.g.,
 CC ligament, tendon, muscle, fibrocartilage, joint capsule and

CC intervertebral discs. The OP-1 mutants can be used to repair diseased or
 CC damaged mammalian tissue and to prevent or substantially inhibit
 CC immune/inflammatory response-mediated tissue damage and scar tissue
 CC formation following an injury. Compared to the wild-type TGF-beta
 CC superfamily members, the mutant proteins have improved in vitro refolding
 CC properties in a pH range of 6-9, increased solubility in aqueous solution
 CC and improved stability and/or activity. Sequences AAB09519-B09542 and
 CC AAB09553-B09558 represent a variety of wild-type TGF-beta superfamily
 CC proteins referred to in the specification
 XX
 XX Sequence 102 AA;

Query Match 42.9%; Score 69; DB 3; Length 102;
 Best Local Similarity 100.0%; Pred. No. 1.6e-57;
 Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 93 CDFPLRSHLEPTNNAIIQTLLNSMAPDAAPASCCVPARLSPISILYIDANNVYKQYED 152
 34 CDFPLRSHLEPTNNAIIQTLLNSMAPDAAPASCCVPARLSPISILYIDANNVYKQYED 93

QY 153 MVEACGCR 161
 94 MVEACGCR 102

RESULT 15
 AAB02824
 ID AAB02824 standard; protein, 102 AA.

AC AAB02824;
 XX
 XX 22-AUG-2000 (first entry)
 DT
 XX Human CDMF-3 construct amino acid sequence SEQ ID NO:88.
 DE
 XX Tumour growth factor beta; TGF-beta; morphogenic protein; BMP; OP;
 KW bone morphogenic protein; osteogenic protein; mutant; modified;
 KW finger 2 sub-domain; finger 1 domain; heel domain; chimeric protein;
 KW osteogenic; proliferative; antiinflammatory; tissue morphogenesis;
 KW tissue repair; regeneration; proliferation; differentiation.
 XX
 OS Homo sapiens.
 XX
 PN W0200020591-A2.
 PD 13-APR-2000.
 PF 07-OCT-1999; 99WO-US023370.
 XX
 PR 07-OCT-1998; 98US-0103418P.
 PR 16-AUG-1999; 99US-00374936.
 XX
 PA (STYC) STRYKER CORP.
 XX
 PI Oppermann H, Tai M, McCartney J;
 DR WPI; 2000-303776/26.

PT Novel TGF-beta superfamily mutant chimeric protein, useful for inducing
 PT tissue morphogenesis in e.g. bone, comprises a dimer consisting of one
 PT monomer containing domains from two family members.
 XX
 PS Disclosure; Page 149; 149pp; English.

CC The present invention describes a tumour growth factor beta (TGF-beta)
 CC superfamily chimeric protein (I) derived from at least 2 different
 CC members of the superfamily comprising a dimer with one monomer that
 CC contains a finger 2 domain derived from a first family member and a
 CC finger 1 domain and heel domain, both derived from a second family
 CC member. The monomer further comprises a conserved C-terminal cysteine
 CC skeleton. (I) has osteogenic, proliferative and antiinflammatory
 CC activities. The TGF-beta superfamily chimeric proteins (I) are useful for
 CC inducing tissue morphogenesis (i.e. molecules capable of tissue repair

CC and regeneration and/or inhibiting inflammation) in bone, non-mineralised
CC skeletal tissue, dental tissue, connective tissue, brain, liver and nerve
CC and for inducing the proliferation and differentiation of uncommitted
CC progenitor cells in a tissue-specific manner to support new tissue
CC formation. AA429887 to AA429897 and AAB02748 to AAB02824 represent
CC sequences used in the exemplification of the present invention
XX

SQ Sequence 102 AA:

Query Match 42.9%; Score 69; DB 3; Length 102;

Best Local Similarity 100.0%; Pred. No. 1.6e-57;

Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 CDPELRSHLEPTNHAIIQTLNLSMAPDAPASCCVPARLSPISILYIDAANNVYKQYED 152
|||
DB 34 CDPELRSHLEPTNHAIIQTLNLSMAPDAPASCCVPARLSPISILYIDAANNVYKQYED 93
|||

QY 153 MVEACGCR 161
|||

DB 94 MVEACGCR 102
|||

Search completed: July 15, 2005, 15:19:01
Job time : 162 secs

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OM protein - protein search, using BW model

Run on: July 15, 2005, 14:59:25 / Search time 173 Seconds

(without alignments)
476.559 Million cell updates/sec

Title: US-10-758-210-6

Perfect score: 880

Sequence: 1 AGSRKANIGCGRRRRRTALAG.....ANNVYKQEDMVVEACGCR 161

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match Length	DB ID	Description
1	880	100.0	461 1 GDF7 MOUSE	P43029 mus musculus
2	712.5	81.0	294 2 Q9BDW9	Q9BDW9 macaca fasc
3	712.5	81.0	447 1 GDF7 CERAE	Q9BDW8 cercopithec
4	712.5	81.0	453 2 Q75RY1	Q75RY1 homo sapien
5	709.5	80.6	450 1 GFD7 HUMAN	Q75RY1 homo sapien
6	574.5	65.3	261 2 Q9W6C0	Q9W6C0 brachydanio
7	568.5	64.6	126 2 Q93573	Q93573 gallus gall
8	557	63.3	452 2 Q6HAI0	Q6HAI0 rattus norv
9	556	63.2	454 2 Q70UT4	Q70UT4 mus musculus
10	553	62.8	201 2 Q6R1S8	Q6R1S8 homo sapien
11	553	62.8	455 2 Q6KFI0	Q6KFI0 homo sapien
12	550	62.5	125 1 GDF6 MOUSE	P43028 mus musculus
13	544	61.8	412 2 Q12938	Q12938 brachydanio
14	540.5	61.4	436 1 GDF6 BOVIN	P55106 bos taurus
15	535	60.8	399 2 Q9W753	Q9W753 xenopus lae
16	526	59.8	413 2 Q9DGN4	Q9DGN4 xenopus lae
17	512	58.2	249 2 Q8BRW9	Q8BRW9 mus musculus
18	512	58.2	495 1 GDF5 MOUSE	P43027 mus musculus
19	512	58.2	500 2 Q9W6G0	Q9W6G0 gallus gall
20	510	58.0	501 1 GDF5 HUMAN	P43026 homo sapien
21	507.5	57.7	494 2 Q68K60	Q68K60 xenopus lae
22	501	56.9	257 2 Q42303	Q42303 brachydanio
23	462	52.5	324 2 Q9YHW9	Q9YHW9 gallus gall
24	426	48.4	621 1 DECA DROPS	P91699 drosophila
25	395	44.9	478 2 Q6J3S4	Q6J3S4 petromyzon
26	394.5	44.8	614 2 P91720	P91720 drosophila
27	391	44.4	277 2 Q9Y882	Q9Y882 lampetra ja
28	386	43.9	588 1 DECA DROME	P07713 drosophila
29	385	43.8	422 2 Q6J3S6	Q6J3S6 petromyzon
30	380.5	43.2	370 2 Q869A4	Q869A4 acaearanea
31	380	43.2	182 2 Q90Y81	Q90Y81 lampetra ja

32	377.5	42.9	178 2 Q25211	Q25211 junonia coe
33	377	42.8	588 2 Q6AMM1	Q6AMM1 drosophila
34	376	42.7	588 2 Q9VOC6	Q9VOC6 drosophila
35	376	42.7	593 1 DECA DROSI	P91706 drosophila
36	375	42.6	411 2 Q9U4I8	Q9U4I8 brachydanio
37	374.5	42.6	361 2 Q96504	Q96504 brachydanio
38	368	41.8	405 2 Q9U5E8	Q9U5E8 psychodera
39	364	41.4	379 2 Q6PUC6	Q6PUC6 anopheles g
40	364	41.4	459 2 Q70307	Q70307 anopheles g
41	363	41.2	289 2 Q9XYG8	Q9XYG8 strongyloc
42	363	41.2	509 2 Q8W5S9	Q8W5S9 archaeter t
43	362	41.1	67 2 Q02784	Q02784 bos taurus
44	362	41.1	399 1 EMB8A_MOUSE	P34821 mus musculus
45	361.5	41.1	204 2 Q9X269	Q9X269 tripneustes

ALIGNMENTS

RESULT 1
GDF7_MOUSE STANDARD. PRT: 461 AA.
ID GDF7_MOUSE
AC P43029; Q7TMX4; Q99W11;
DT 01-NOV-1995 (Rel. 32, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Growth/differentiation factor 7 precursor (GDF-7).
GN Name=Gdf7; Synonyms=Gdf-7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=BALB/c; TISSUE=Testis;
RA Guo J.H., Yu L.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-441 FROM N.A. (ISOFORM 1).
RC STRAIN=TT2;
RX Watanabe A., Fujita H., Hayashi M., Yamamori T.;
RA "Growth/differentiation factor 7 is preferentially expressed in the
RT primary motor area of the monkey neocortex."
RL J. Neurochem. 76:1455-1464(2001).
RN [3]
RP SEQUENCE OF 311-461 FROM N.A.
RC STRAIN=BALB/c; TISSUE=Liver;
RX MEDLINE=94195427; PubMed=8145850; DOI=10.1038/368639a0;
RA Storm E.E., Huynh T.V., Copeland N.G., Jenkins N.A., Kingsley D.M.,
Lee S.-J.;
RA "Limb alterations in brachypodism mice due to mutations in a new
RT member of the TGF beta-superfamily."
RL Nature 368:639-643(1994).
RN [4]
RP SUBMIT: Homodimer; disulfide-linked (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P43029-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P43029-2; Sequence=VSP_010764;
CC -!- SIMILARITY: Belongs to the TGF-beta family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF525752; AAP97721.1; -
CC EMBL; AF254571; AAK30843.1; -

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DR EMBL; AF254570; AAK30843.1; JOINED.
DR EMBL; U08339; AAI18780.1; -.
DR PIR; S43296; S43296.
DR HSSP; P12643; 3BMP.
DR MGD; MGI:95690; Gdf7.
DR GO; GO:0005576; C:extracellular; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007411; P:axon guidance; IDA.
DR InterPro; IPR002400; GF_cyknct.
DR InterPro; IPR002405; Inhibin_alpha.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF_beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
DR Alternative splicing; CytoKine; Glycoprotein; Growth factor; Signal.
KM SIGNAL 1 19 Potential.
FT PROPEP 20 315 Potential.
FT CHAIN 316 461 Growth/differentiation factor 7.
FT DISULFD 360 426 By similarity.
FT DISULFD 389 458 By similarity.
FT DISULFD 393 460 By similarity.
FT DISULFD 425 425 Interchain (By similarity).
FT DOMAIN 311 315 Poly-Arg.
FT DOMAIN 326 351 Poly-Gly.
FT CARBOXD 79 79 N-linked (GlcNAc... ) (Potential).
FT VASPLIC 123 130 Missing (in isoform 2).
SQ SEQUENCE 461 AA; 47890 MW; 92C2511C8EDE478 CRC64;

Query Match 100.0%; Score 880; DB 1; Length 461;
Best Local Similarity 100.0%; Pred. No. 1.6e-57;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGSRKANIGRRRRRTALAGTGAAGSGGGGGGGGGGGGGGAGRGHGRGRSRC 60
DB 301 AGSRKANIGRRRRRTALAGTGAAGSGGGGGGGGGGGGGGAGRGHGRGRSRC 360
QY 61 SRKSLHVPKELGMDWIIAPLDYEAHCEGVCDFPLRSHLEPTNHAIQTLLNSMAPDA 120
DB 361 SRKSLHVPKELGMDWIIAPLDYEAHCEGVCDFPLRSHLEPTNHAIQTLLNSMAPDA 420
QY 121 APASCCVPARLSPISILYIDAANNVVKQYEDMVVEACGCR 161
DB 421 APASCCVPARLSPISILYIDAANNVVKQYEDMVVEACGCR 461

RESULT 2
Q9BDM9 PRELIMINARY; PRT; 294 AA.
AC Q9BDM9;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Growth/differentiation factor 7 (Fragment).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OC NCBI_TaxID=9541;
OX [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Cerebral cortex motor area;
RC MEDLINE=21136583; PubMed=11238730;
RA Matakabe A., Fujita H., Hayashi M., Yamamori T.;
RT "Growth/differentiation factor 7 is preferentially expressed in the
RT primary motor area of the monkey neocortex.";
RL J. Neurochem. 76:1455-1464(2001)
CC -1- SIMILARITY: Belongs to the TGF-beta family.
DR EMBL; AF254567; AAK27794.1; -.
DR HSSP; P12643; 3BMP.
GO; GO:0008083; F:growth factor activity; IEA.

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DR InterPro; IPR002400; GF_cyknct.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF_beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
DR Growth factor.
FT NON TER 1 1
SQ SEQUENCE 294 AA; 31792 MW; 49B7BCD9F27A39F CRC64;

Query Match 81.0%; Score 712.5; DB 2; Length 294;
Best Local Similarity 85.0%; Pred. No. 2.8e-45;
Matches 136; Conservative 1; Mismatches 6; Indels 17; Gaps 1;

QY 2 GSRKANIGRRRRRTALAGTGAAGSGGGGGGGGGGGGGGAGRGHGRGRSRC 61
DB 152 GSPRAVATGRRRRRTALAGTGAAGS-----GGGAGRGHGRGRSRC 194
QY 62 RKSLLHVPKELGMDWIIAPLDYEAHCEGVCDFPLRSHLEPTNHAIQTLLNSMAPDA 121
DB 195 RKSLLHVPKELGMDWIIAPLDYEAHCEGVCDFPLRSHLEPTNHAIQTLLNSMAPDA 254
QY 122 PASCVCVPARLSPISILYIDAANNVVKQYEDMVVEACGCR 161
DB 255 PASCVCVPARLSPISILYIDAANNVVKQYEDMVVEACGCR 294

RESULT 3
GDF7_CERAE STANDARD; PRT; 447 AA.
ID GDF7_CERAE;
AC Q9BDM9;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Growth/differentiation factor 7 precursor (GDF-7).
GN Name=GDF7;
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Cercopitheidae.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A. AND TISSUE SPECIFICITY.
RX MEDLINE=21136583; PubMed=11238730;
RA Matakabe A., Fujita H., Hayashi M., Yamamori T.;
RT "Growth/differentiation factor 7 is preferentially expressed in the
RT primary motor area of the monkey neocortex.";
RL J. Neurochem. 76:1455-1464(2001).
CC -1- FUNCTION: May play an active role in the motor area of the primate
CC neocortex.
CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -1- TISSUE SPECIFICITY: Highly expressed in the primary aera of brain
CC neocortex.
CC -1- SIMILARITY: Belongs to the TGF-beta family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF254569; AAK30842.1; -.
DR EMBL; AF254568; AAK30842.1; JOINED.
DR HSSP; P12643; 3BMP.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF_beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.

```

DR PROSITE; PS00250; TGF_BETA_1; 1.
 KM Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 19 Potential.
 FT PROPEP 20 318 Potential.
 FT CHAIN 319 447 Growth/differentiation factor 7.
 FT DISULFID 346 412 By similarity.
 FT DISULFID 375 444 By similarity.
 FT DISULFID 379 446 By similarity.
 FT DISULFID 411 411 Interchain (By similarity).
 FT CARBOHYD 80 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 447 AA; 4686 MM; DP46D591925A8391 CRC64;
 Query Match 81.0%; Score 712.5; DB 1; Length 447;
 Best Local Similarity 85.0%; Pred. No. 4.1e-45;
 Matches 136; Conservative 1; Mismatches 6; Indels 17; Gaps 1;
 QY 2 GSRKALGRRRRRTALAGTGAQGGGGGGGGGGGGGGGAGRGHGRSRCS 61
 DB 305 GSPRAVTAAGRRRRRTALAGTGAQGS-----GGAGRGHGRSRCS 347
 QY 62 RKSILHVDPEKLGMDWMIAPLDYEAYHCEGVCDFPLRSHLEPTNNAIIQTLLNSMAPDAP 121
 DB 348 RKLHVDPEKLGMDWMIAPLDYEAYHCEGVCDFPLRSHLEPTNNAIIQTLLNSMAPDAP 407
 QY 122 PASCVPARLSPISILYIDAANNVYKQYEDMVVEACGCR 161
 DB 408 PASCVPARLSPISILYIDAANNVYKQYEDMVVEACGCR 447
 RESULT 4
 ID Q75RY1 PRELIMINARY; PRT; 453 AA.
 AC Q75RY1
 DT 05-JUL-2004 (TRENBLREL. 27, Created)
 DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
 DE 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
 DE Growth differentiation factor 7.
 GN Name=gdf7;
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Suzuki M., Shimokawa H., Kasugai S.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
 DR EMBL; AB158468; BAD07014.1; -.
 DR HSPB; P01137; IKLA.
 DR GO; GO:0008083; P:growth factor activity; IEA.
 DR GO; GO:0040007; P:growth; IEA.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR Pfam; PF00019; TGF_beta.1.
 DR ProDom; PD000357; TGFb.1.
 DR SMART; SM00204; TGFb.1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KM Growth factor.
 SQ SEQUENCE 453 AA; 47121 MM; 9FD8CB759C63DFID CRC64;
 Query Match 81.0%; Score 712.5; DB 2; Length 453;
 Best Local Similarity 84.9%; Pred. No. 4.2e-45;
 Matches 135; Conservative 3; Mismatches 4; Indels 17; Gaps 1;
 QY 3 SRKANLGRRRRRTALAGTGAQGGGGGGGGGGGGGGGAGRGHGRSRCS 62
 DB 312 SPRAVIGRRRRRTALAGTGAQGS-----GGAGRGHGRSRCS 354
 QY 63 KSLHVDPEKLGMDWMIAPLDYEAYHCEGVCDFPLRSHLEPTNNAIIQTLLNSMAPDAP 122
 DB 355 KPLHVDPEKLGMDWMIAPLDYEAYHCEGVCDFPLRSHLEPTNNAIIQTLLNSMAPDAP 414

QY 123 ASCCVPARLSPISILYIDAANNVYKQYEDMVVEACGCR 161
 DB 415 ASCCVPARLSPISILYIDAANNVYKQYEDMVVEACGCR 453
 RESULT 5
 ID GPD7 HUMAN STANDARD; PRT; 450 AA.
 AC G724P5;
 DT 25-OCT-2004 (Rel. 45, Created).
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Growth/differentiation factor 7 precursor (GDF-7).
 GN Name=GDF7;
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Guo J.H., Yu L.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: May play an active role in the motor area of the primate neocortex (By similarity).
 CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
 CC -----
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 CC -----
 DR EMBL; AF523269; AAP97720.1; -.
 DR Genew; HGNC:4222; GDF7.
 DR MIM; 604651; -.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00019; TGF_beta.1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR ProDom; PD000357; TGFb.1.
 DR SMART; SM00204; TGFb.1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KM Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 19 Potential.
 FT PROPEP 20 321 Potential.
 FT CHAIN 322 450 Growth/differentiation factor 7.
 FT DISULFID 349 415 By similarity.
 FT DISULFID 378 447 By similarity.
 FT DISULFID 382 449 By similarity.
 FT DISULFID 414 414 Interchain (By similarity).
 FT CARBOHYD 83 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 450 AA; 46966 MM; CDB4C617685037BD CRC64;
 Query Match 80.6%; Score 709.5; DB 1; Length 450;
 Best Local Similarity 84.3%; Pred. No. 6.9e-45;
 Matches 134; Conservative 4; Mismatches 4; Indels 17; Gaps 1;
 QY 3 SRKANLGRRRRRTALAGTGAQGGGGGGGGGGGGGGGAGRGHGRSRCS 62
 DB 309 SPRAVIGRRRRRTALAGTGAQGS-----GGAGRGHGRSRCS 351
 QY 63 KSLHVDPEKLGMDWMIAPLDYEAYHCEGVCDFPLRSHLEPTNNAIIQTLLNSMAPDAP 122
 DB 352 KPLHVDPEKLGMDWMIAPLDYEAYHCEGVCDFPLRSHLEPTNNAIIQTLLNSMAPDAP 411
 QY 123 ASCCVPARLSPISILYIDAANNVYKQYEDMVVEACGCR 161
 DB 412 ASCCVPARLSPISILYIDAANNVYKQYEDMVVEACGCR 450

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RESULT 6
O9M6CO PRELIMINARY; PRT; 261 AA.
ID O9M6CO
AC O9M6CO;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Growth/differentiation factor 7 (Fragment).
GN Name=gdf7;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=99148135; PubMed=10022976;
RA Davidson A.J., Postlethwait J.H., Yan Y.L., Beier D.R., van Doren C.,
RA Poernaler D., Celeste A.J., Crosier K.E., Crosier P.S.;
RT "Isolation of zebrafish gdf7 and comparative genetic mapping of genes
RT belonging to the growth/differentiation factor 5, 6, 7 subgroup of the
RT TGF-beta superfamily."
RL Genome Res. 9:121-129 (1999).
CC -1- SIMILARITY: Belongs to the TGF-beta family.
DR HSSP; P08476; INYU.
DR ZFIN; ZDB-GENE-990714-1; gdf7.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR InterPro; IPR002400; F:cell growth and/or maintenance; IEA.
DR InterPro; IPR002405; Inhibin_alpha.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF_beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRODOM; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KM Growth factor.
FT NON TER
SQ SEQUENCE 261 AA; 29414 MM; 77346B977036A104 CRC64;

Query Match 65.3%; Score 574.5; DB 2; Length 261;
Best Local Similarity 70.9%; Pred. No. 4.3e-35;
Matches 107; Conservative 10; Mismatches 15; Indels 19; Gaps 1;

QY 11 RRRRTTLAGTGAQSGGGGGGGGGGGGGGGGGAGRGHGRGRSRCSRLHYDFK 70
DB 130 RRRRTTLAGRPGVGPITSGGKG-----RRTRGCRKRLHNVFK 170
QY 71 ELGWDWIIAPLDYEAVHCGVCDPPLRSHLEPTNHAIIQTLLNSMAPDAAPASCVPAR 130
DB 171 ELGWDWIIAPLDYEAVHCGVCDPPLRSHLEPTNHAIIQTLLNSMAPDPESTPSCVPSK 230
QY 131 LSPISILYIDANNVVKQYEDMVVEACGR 161
DB 231 LSPISILYIDSGNNVVTKQYEDMVVEACGR 261

RESULT 7
O93573 PRELIMINARY; PRT; 126 AA.
ID O93573
AC O93573;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Putative growth/differentiation factor 6/7 (Fragment).
GN Name=GDF6/7;
OS Gallus gallus (chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99026113; PubMed=9808626;
RA Lee K.J., Mendelsohn M., Jessell T.M.;
RT "Neuronal patterning by BMPs: a requirement for GDF7 in the generation
RT of a discrete class of commissural interneurons in the mouse spinal
RT cord."
RL Genes Dev. 12:3394-3407 (1998).
CC -1- SIMILARITY: Belongs to the TGF-beta family.
DR EMBL; AF089086; AAC97113.1; -.
DR HSSP; P08476; INYU.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR002405; Inhibin_alpha.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF_beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRODOM; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KM Growth factor.
FT NON TER
SQ SEQUENCE 126 AA; 14265 MM; CB824D280F44A394 CRC64;

Query Match 64.6%; Score 568.5; DB 2; Length 126;
Best Local Similarity 67.5%; Pred. No. 6.3e-35;
Matches 102; Conservative 13; Mismatches 11; Indels 25; Gaps 1;

QY 11 RRRRTTLAGTGAQSGGGGGGGGGGGGGGGGGAGRGHGRGRSRCSRLHYDFK 70
DB 1 RRRRTTIIARSG-----GGHGKAKKTRCSRLPLHNVFK 35
QY 71 ELGWDWIIAPLDYEAVHCGVCDPPLRSHLEPTNHAIIQTLLNSMAPDAAPASCVPAR 130
DB 36 ELGWDWIIAPLDYEAVHCGVCDPPLRSHLEPTNHAIIQTLLNSMAPDPESTPSCVPSK 95
QY 131 LSPISILYIDANNVVKQYEDMVVEACGR 161
DB 96 LSPISILYIDSGNNVVTKQYEDMVVEACGR 126

RESULT 8
O6HA10 PRELIMINARY; PRT; 452 AA.
ID O6HA10
AC O6HA10;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Growth/differentiation factor 16.
GN Name=gdf16;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A.
RA STRAIN=Sprague-Dawley; TISSUE=Brain;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the TGF-beta family.
DR EMBL; AJ537426; CAD60936.2; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR GO; GO:0040007; P:growth; IEA.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR002405; Inhibin_alpha.
DR InterPro; IPR001839; TGFb.
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DR InterPro: IPR001111; TGFb_N.
 DR Pfam: PF00688; TGFb_propeptide; 1.
 DR Pfam: PF00019; TGF_beta; 1.
 DR PRINTS: PR00438; GFCYSKNOT.
 DR PRINTS: PR00669; INHIBINA.
 DR PRODOM: PD000357; TGFb; 1.
 DR SMART: SM00204; TGFb; 1.
 DR PROSITE: PS00250; TGF_BETA_1; 1.
 DR Growth factor.
 KM SEQUENCE 452 AA; 51013 MM; DF75687584C1B52A CRC64;

Query Match 63.3%; Score 557; DB 2; Length 452;
 Best Local Similarity 67.1%; Pred. No. 1.4e-33;
 Matches 102; Conservative 11; Mismatches 13; Indels 26; Gaps 1;

QY 10 GRRRRRTLAATRGAGSGGGGGGGGGGGGGGGGAGRGHGRGRSRSRSLHVF 69
 DB 327 GRRRRRTLAATRGAGSGGGGGGGGGGGGGGGGAGRGHGRGRSRSRSLHVF 360
 QY 70 KELGMDWIIAPLVEAYHCGVCDPPLRSHLEPTNNAIIOTLNSMAPDAPASCVA 129
 DB 361 KELGMDWIIAPLVEAYHCGVCDPPLRSHLEPTNNAIIOTLNSMAPDAPASCVA 420
 QY 130 RLSPISILYIDANNVYKQYEDMVVEACGR 161
 DB 421 KLTPISILYIDAGNNVYKQYEDMVVEACGR 452

RESULT 9

ID Q70UT4 PRELIMINARY; PRT; 454 AA.

AC Q70UT4
 DT 05-JUL-2004 (TREMblrel. 27, Created)
 DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
 DE Growth differentiation factor 16.
 GN Name=GDFF16;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Kunming; TISSUE=Brain;
 RA Guo J.H.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
 DR HSBP; P01137; IKLA.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0008083; F:growth factor activity; IEA.
 DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
 DR GO; GO:0040007; P:growth; IEA.
 DR InterPro: IPR002400; GF_cysknct.
 DR InterPro: IPR002405; Inhibin_alpha.
 DR InterPro: IPR001839; TGFb.
 DR InterPro: IPR001111; TGFb_N.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR Pfam; PF00019; TGF_beta; 1.
 DR PRINTS: PR00438; GFCYSKNOT.
 DR PRINTS: PR00669; INHIBINA.
 DR PRODOM: PD000357; TGFb; 1.
 DR SMART: SM00204; TGFb; 1.
 DR PROSITE: PS00250; TGF_BETA_1; 1.
 DR Growth factor.
 KM SEQUENCE 454 AA; 50941 MM; 5A3FADDA539CB38 CRC64;

Query Match 63.2%; Score 556; DB 2; Length 454;
 Best Local Similarity 67.1%; Pred. No. 1.6e-33;
 Matches 102; Conservative 10; Mismatches 14; Indels 26; Gaps 1;
 QY 10 GRRRRRTLAATRGAGSGGGGGGGGGGGGGGGGAGRGHGRGRSRSRSLHVF 69
 DB 327 GRRRRRTLAATRGAGSGGGGGGGGGGGGGGGGAGRGHGRGRSRSRSLHVF 360

DB 329 GRRRRRTAFASRH-----GRRHKKRRLRCSRKLHVF 362
 QY 70 KELGMDWIIAPLVEAYHCGVCDPPLRSHLEPTNNAIIOTLNSMAPDAPASCVA 129
 DB 363 KELGMDWIIAPLVEAYHCGVCDPPLRSHLEPTNNAIIOTLNSMAPDAPASCVA 422
 QY 130 RLSPISILYIDANNVYKQYEDMVVEACGR 161
 DB 423 KLTPISILYIDAGNNVYKQYEDMVVEACGR 454

RESULT 10

ID Q6P158 PRELIMINARY; PRT; 201 AA.

AC Q6P158
 DT 05-JUL-2004 (TREMblrel. 27, Created)
 DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
 DE LOC392255 protein (Fragment).
 GN Name=LOC392255;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feltingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshitsuki S., Catinici P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,
 RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman W., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grilwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzyzanski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Maitra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Strauberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
 DR EMBL; BC043222; AAH43222.1; -.
 DR HSBP; P01137; IKLA.
 DR GO; GO:0008083; F:growth factor activity; IEA.
 DR InterPro: IPR002400; GF_cysknct.
 DR InterPro: IPR001839; TGFb.
 DR Pfam; PF00019; TGF_beta; 1.
 DR PRINTS: PR00438; GFCYSKNOT.
 DR PRODOM: PD000357; TGFb; 1.
 DR SMART: SM00204; TGFb; 1.
 DR PROSITE: PS00250; TGF_BETA_1; 1.
 DR Growth factor.
 KM SEQUENCE 201 AA; 22441 MM; FF1BD52EBE0517A CRC64;

Query Match 62.8%; Score 553; DB 2; Length 201;
 Best Local Similarity 66.4%; Pred. No. 1.3e-33;
 Matches 101; Conservative 11; Mismatches 14; Indels 26; Gaps 1;
 QY 10 GRRRRRTLAATRGAGSGGGGGGGGGGGGGGGGAGRGHGRGRSRSRSLHVF 69
 DB 329 GRRRRRTAFASRH-----GRRHKKRRLRCSRKLHVF 362

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Db      76 GRRRRRTAFASRH-----GRHGGKSRRLRCSKPPHLVNF 109
Qy      70 KELGMDWIIAPLPEYEAHCGVCDPPLRSHLEPTNNAIIOTLNSMAPDAPASCCVPA 129
Db      110 KELGMDWIIAPLPEYEAHCGVCDPPLRSHLEPTNNAIIOTLNSMDPGSTPPSCCVPT 169
Qy      130 RLSPISILYIDANNVYKQYEDMVVEACGCR 161
Db      170 KLTPTISILYIDAGNNVYKQYEDMVVEACGCR 201

RESULT 11
ID 06KF10 PRELIMINARY; PRT; 455 AA.
AC 06KF10
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Growth differentiation factor 16.
GN Name=GDF16;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hind brain;
RA Guo J.H.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the TGF-beta family.
DR EMBL; AJ537424; CAD60934.1; -.
DR HSSP; P01137; IALA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0040007; P:growth; IEA.
DR InterPro; IPR002400; GF_cyknct.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR Pfam; PF00019; TGF_beta; 1.
DR PRINTS; PR00438; GF_CYS_KNOT.
DR PRODOM; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KM Growth factor.
SQ SEQUENCE 455 AA; 50661 MW; F9F365B99E8C659C CRC64;

Query Match 62.8%; Score 553; DB 2; Length 455;
Best Local Similarity 66.4%; Pred. No. 2.7e-33;
Matches 101; Conservative 11; Mismatches 14; Indels 26; Gaps 1;

Qy      10 GRRRRRTAFASRH-----GRHGGKSRRLRCSKPPHLVNF 69
Db      330 GRRRRRTAFASRH-----GRHGGKSRRLRCSKPPHLVNF 363
Qy      70 KELGMDWIIAPLPEYEAHCGVCDPPLRSHLEPTNNAIIOTLNSMAPDAPASCCVPA 129
Db      364 KELGMDWIIAPLPEYEAHCGVCDPPLRSHLEPTNNAIIOTLNSMDPGSTPPSCCVPT 423
Qy      130 RLSPISILYIDANNVYKQYEDMVVEACGCR 161
Db      424 KLTPTISILYIDAGNNVYKQYEDMVVEACGCR 455

RESULT 12
ID 06F6 MOUSE STANDARD; PRT; 125 AA.
AC 06F6
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Growth/differentiation factor 6 precursor (GDF-6) (Fragment).
GN Name=Gdf6; Synonyms=Gdf-6;

```

```

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Liver;
RX MEDLINE=94195427; Pubmed=8145850; DOI=10.1038/368639a0;
RA Storm E.E., Huynh T.V., Copeland N.G., Jenkins N.A., Kingsley D.M.,
RT Lee S.-J.;
RT "Limb alterations in brachypodism mice due to mutations in a new
member of the TGF beta superfamily."
RL Nature 368:639-643(1994).
CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -1- SIMILARITY: Belongs to the TGF-beta family.
-----
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DR EMBL; U08338; AAA18779.1; -.
DR PIR; S43295; S43295.
DR HSSP; P08476; INYU.
DR MGD; MGI:95689; Gdf6.
DR InterPro; IPR002400; GF_cyknct.
DR InterPro; IPR002405; Inhibin_alpha.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF_beta; 1.
DR PRINTS; PR00438; GF_CYS_KNOT.
DR PRINTS; PR00669; INHIBINA.
DR PRODOM; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KM Cytokine; Glycoprotein; Growth factor.
FT NON TER 1
FT PROPEP <1 5 Potential.
FT CHAIN 6 125 Growth/differentiation factor 6.
FT DISULFID 24 90 By similarity.
FT DISULFID 53 122 By similarity.
FT DISULFID 57 124 By similarity.
FT DISULFID 89 89 Interchain (By similarity).
SQ SEQUENCE 125 AA; 14373 MW; 10FA2A5B748DA32 CRC64;

Query Match 62.5%; Score 550; DB 1; Length 125;
Best Local Similarity 66.9%; Pred. No. 1.5e-33;
Matches 101; Conservative 10; Mismatches 14; Indels 26; Gaps 1;

Qy      11 RRRRRRTAFASRH-----GRHGGKSRRLRCSKPPHLVNF 70
Db      1 RRRRRRTAFASRH-----GRHGGKSRRLRCSKPPHLVNF 34
Qy      71 ELGMDWIIAPLPEYEAHCGVCDPPLRSHLEPTNNAIIOTLNSMAPDAPASCCVPA 130
Db      35 ELGMDWIIAPLPEYEAHCGVCDPPLRSHLEPTNNAIIOTLNSMDPGSTPPSCCVPTK 94
Qy      131 LSPISILYIDANNVYKQYEDMVVEACGCR 161
Db      95 LTPISILYIDAGNNVYKQYEDMVVEACGCR 125

RESULT 13
ID 012938 PRELIMINARY; PRT; 412 AA.
AC 012938
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Dynam protein precursor.
GN Name=gdf6b; Synonyms=dynamo;

```


RX MEDLINE=95050604; PubMed=7951761, Vukicavic S., Luyten F.P.,
RA Chang S., Hoang B., Thomas J.T.,
RA Ryba N.J.P., Kozak C.A., Redd A.H., Moos M.;
RT "Cartilage-derived morphogenetic proteins. New members of the
RT transforming growth factor-beta superfamily predominantly expressed in
RT long bones during human embryonic development.";
RL J. Biol. Chem. 269:28227-28234(1994).
CC -SUBUNIT: Homodimer; disulfide-linked (by similarity).
CC -SIMILARITY: Belongs to the TGF-beta family.

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DR EMBL, U13661, AAA61416.1; -.
DR PIR, B55452; B55452.
DR HSSP, P08476; INYU.
DR InterPro: IPR009056; Cytochrome_C.
DR InterPro: IPR002400; GP_cybknot.
DR InterPro: IPR001839; TGFB_N.
DR InterPro: IPR001111; TGFB_N.
DR Pfam, PF00019; TGF_beta_1.
DR Pfam, PF00688; TGF_propeptide; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PRODOM: PD000357; TGFB_1.
DR SMART: SM00204; TGFB_1.
DR CYTOITE; PS00250; TGF_BETA_1; 1.
KW Cycokine; Glycoprotein; Growth factor.
FT FT NON TER 1 1
FT PROFEP <1 316 Potential.
FT CHAIN 317 436 Growth/differentiation factor 6.
FT DISULFID 335 401 By similarity.
FT DISULFID 364 433 By similarity.
FT DISULFID 368 435 By similarity.
FT DISULFID 400 400 Interchain (By similarity).
FT CARBOHYD 27 27 N-linked (GlcNAc...) (Potential).
FT FT CARBOHYD 89 89 N-linked (GlcNAc) (Potential).
SQ SEQUENCE 436 AA; 47873 MW; B068BE1ZBFBAE91D CRC64;

Query Match 61.4%; Score 540.5; DB 1; Length 436;
Best Local Similarity 57.8%; Pred. No. 2.2e-32;
Matches 104; Conservative 15; Mismatches 32; Indels 29; Gaps 2

CY 11 RRRRRTLAACTGAQSGGGGGGGGGGGGG--GGCGA-----48
 |::||:
DB 257 RSORKTLFAEMREGLGSATEVVGCGAGESGPPEPPPSGTPDAGLTWSPSGRRR 316

CY 49 -----GRHGHRGRSRCSRKSLHVFKELGMDWTIAPLDVAHYHCVCDPPLASHL 101
 ||||:|::|:
DB 317 TAPAASRGKHGHCKSKLRICKPLHFVKELGMWDWIITALEZYAHCEGCDFPLLNSHL 376

CY 102 EPTTHAIITQLNLNMAADAPASCVCVPARISSIPISIIYIDAANNVVYQVEDMVVEACGR 161
 ||||:|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~::~|||:
CY XENOPUSLAIOQLTNMSMDCGSTFPSCCVPTKLTPISILIYTDAIGNNVYNIEYMVESGCCCR 436
 377 EPFNHAIIQTLMNSMDCGSTFPSCCVPTKLTPISILIYTDAIGNNVYNIEYMVESGCCCR 436

RESULT 15
OSNM753 PRELIMINARY; PRT; 399 AA.

ID OSNM753 AC OSNM753; ID OSNM753; PT; 399 AA.
DT 01-NOV-1999 (TREMBLErel. 12, Created)
DT 01-NOV-1999 (TREMBLErel. 12, Last sequence update)
DT 01-MAR-2004 (TREMBLErel. 26, Last annotation update)
DE Growth and differentiation factor 6.
GN Name=GDF6;
OC Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.

OX NCB1_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99396700; PubMed=10393114;
RA Chang C, Hemmati-Britvanlou A.;
RT "Xenopus GDF6, a new antagonist of noggin and a partner of BMPs.";
RL Development 126:3347-3357(1999).
CC -1- SIMILARITY: Belong to the TGF-beta family.
DR EMBL; AF155125; AAD38402.1; -.
DR HSSP; P08476; INTU.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR GO; GO:0040007; P:growth; IEA.
DR DR InterPro; IPR002400; GF_cyknoc.
DR DR InterPro; IPR002405; Inhibin_alpha.
DR DR InterPro; IPR001839; TGFb.
DR DR InterPro; IPR001111; TGFb N.
DR DR Pfam; PF00688; TGFb_propeptide; 1.
DR DR Pfam; PF00019; TGF_beta_1.
DR DR PRINTS; PR00438; GFCTSKNOT.
DR DR PRINTS; PR00669; INHIBINOT.
DR DR Prodom; PD000357; TGFb; 1.
DR DR SMART; SM00204; TGFb; 1.
DR DR PROSITE; PS00250; TGF_beta_1; 1.
KM Growth factor.
SQ SEQUENCE 399 AA; 45571 MW; C549D973B508B517 CRC64;

C; Superfamily: Inhibin

A;Cross-references: UNIPROT:P43029; GB:U08339; NID:g488465; PIDN:AAA18780.1; PID:g48846
 C;Superfamily: inhibin
 Query Match 94.3%; Score 830; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 2,3e-61;
 Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 RRRRRTLAAGRGAGSGGGGGGGGGGGGGGGGAGRGHGRGRGRCSRKSLHYDFK 70
 1 RRRRRTLAAGRGAGSGGGGGGGGGGGGGGGGAGRGHGRGRGRCSRKSLHYDFK 60
 QY 71 ELGWDWIIALPDYEAHCEGVCDPLRSLHLEPTNHAIIQTLLNSMAPDAAPASCCVPAR 130
 Db 61 ELGWDWIIALPDYEAHCEGVCDPLRSLHLEPTNHAIIQTLLNSMAPDAAPASCCVPAR 120
 QY 131 LSPISILYIDANNVVKQYEDMVEACGR 161
 Db 121 LSPISILYIDANNVVKQYEDMVEACGR 151
 RESULT 2
 S43295
 bone morphogenetic protein homolog GDF6 precursor - mouse (fragment)
 N;Alternate names: growth and differentiation factor 6
 C;Species: Mus musculus (house mouse)
 C;Date: 20-Oct-1994 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004
 C;Accession: S43295
 R;Storm, E.E.; Huvn, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingstley, D.M.; Lee, S.J.
 Nature 368, 639-643, 1994
 A;Title: Lmb alterations in brachypodism mice due to mutations in a new member of the
 A;Reference number: S43294; MUID:94195427; PMID:8145850
 A;Molecule type: DNA
 A;Accession: S43295
 A;Cross-references: UNIPROT:P43028; EMBL:U08338; NID:g488463; PIDN:AAA18779.1; PID:g48846
 C;Genetics
 A;Gene: Gdf6
 A;Superfamily: inhibin

A:Gene: GDB:BMP4; BMP2B
 A:Cross-references: GDB:125205; OMIM:112262
 A:Map position: 14q22-14q23
 C:Superfamily: inhibin
 C:Keywords: bone; glycoprotein
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-292/Domain: propeptide #status predicted <PRO>
 F:293-408/Product: bone morphogenetic protein 4 #status predicted <MAT>
 F:143,208,350,365/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 39.9%; Score 351.5; DB 1; Length 408;
 Best Local Similarity 49.3%; Pred. No. 1.2e-21;
 Matches 66; Conservative 20; Mismatches 29; Indels 19; Gaps 3;

QY 46 GGAGRGH-----GSRKSLHYDFKELGMDMTIAPLDYEAY 87
 DB 276 GHGGRGHTLRRRAKSPKHHSGRAKKKNCRRHSLYDFSGVGNMDIIVAPRGYQAF 335
 QY 88 HCEGVCDPFLRSHLEPTNHAIIQTLLNSMAPDAAPASCVPARLSPISIIYIDANNVY 147
 DB 336 YCHGDCPFLADHINSTNHAIVQTLVNSV-SSIFPKACVPTLSAISMLYIDEDYKVL 394
 QY 148 QYEDMVVEACGCR 161
 DB 395 NYQEMVVEGCGCR 408

RESULT 11
 A45056
 osteogenic protein 2 precursor - human
 N:Alternate names: bone morphogenetic protein 8; OP-2
 C:Species: Homo sapiens (man)
 C>Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C:Accession: A45056
 R:Ozekaynak, E.; Schlegelberg, P.N.; Jin, D.F.; Clifford, G.M.; Warren, F.D.; Drier, E.
 J. Biol. Chem. 267, 25220-25227, 1992
 A:Title: Osteogenic protein-2. A new member of the transforming growth factor-beta super
 A:Reference number: A45056; PMID:93094231; PMID:1460021
 A:Accession: A45056
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-402 <OK>
 A:Cross-references: UNIPROT:P34820; GB:M97016; NID:g189389; PIDN:AB01360.1; PID:g189390
 A:Experimental source: hippocampus
 A:Note: sequence extracted from NCBI backbone (NCBIRP:120189)
 C:Genetics:
 A:Gene: GDB:BMP8; OP-2
 A:Cross-references: GDB:136392
 C:Superfamily: inhibin

Query Match 39.9%; Score 351; DB 2; Length 402;
 Best Local Similarity 53.2%; Pred. No. 1.2e-21;
 Matches 58; Conservative 22; Mismatches 29; Indels 0; Gaps 0;

QY 52 HGRGRSRSRKSILHYDFKELGMDMTIAPLDYEAYHCEGVCDPFLRSHLEPTNHAIIQT 111
 DB 293 HGRGRGTVLRRAKSPKHHSGRAKKKNCRRHSLYDFSGVGNMDIIVAPRGYQAF 335
 QY 112 LNSMAPDAAPASCVPARLSPISIIYIDANNVYQYEDMVVEACGC 160
 DB 353 LVHLMKNVAVKACCAFTKLSATSVLYSSNNVILKRHRMVKACGC 401

RESULT 12
 S38343
 bone morphogenetic protein 4 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C:Accession: S38343; S33773
 R:Chen, D.; Feng, J.Q.; Feng, M.; Harris, M.A.; Mundy, G.R.; Harris, S.E.
 Biochim. Biophys. Acta 1174, 289-292, 1993
 A:Title: Cloning and sequence of bone morphogenetic protein 4 cDNA from fetal rat calvar
 A:Reference number: S38343; PMID:93385158; PMID:8373807

A:Accession: S38343
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-408 <CHE>
 A:Cross-references: UNIPROT:Q06826; EMBL:Z22607; NID:g296855; PIDN:CAA80329.1; PID:g296
 C:Superfamily: inhibin

Query Match 39.9%; Score 351; DB 2; Length 408;
 Best Local Similarity 48.1%; Pred. No. 1.2e-21;
 Matches 64; Conservative 19; Mismatches 32; Indels 18; Gaps 2;

QY 46 GGAGRGH-----GRRGRSRSRKSILHYDFKELGMDMTIAPLDYEAYH 88
 DB 277 GHGGRGHTLRRRAKSPKHHSGRAKKKNCRRHSLYDFSGVGNMDIIVAPRGYQAF 336
 QY 89 CEGVCDPFLRSHLEPTNHAIIQTLLNSMAPDAAPASCVPARLSPISIIYIDANNVYK 148
 DB 337 CHGDCPFLADHINSTNHAIVQTLVNSV-SSIFPKACVPTLSAISMLYIDEDYKVL 395
 QY 149 QYEDMVVEACGCR 161
 DB 396 NYQEMVVEGCGCR 408

RESULT 13
 I49541
 bone morphogenetic protein 4 - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C:Accession: I49541; S29523; B34201
 R:Feng, J.Q.; Chen, D.; Cooney, A.J.; Tsai, M.; Harris, M.A.; Tsai, S.Y.; Feng, M.; Mun
 J. Biol. Chem. 270, 28364-28373, 1995
 A:Title: The mouse bone morphogenetic protein-4 (BMP-4) gene: Analysis of promoter utilitz.
 A:Reference number: I49541; PMID:96081880; PMID:7499338
 A:Accession: I49541
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-420 <RES>
 A:Cross-references: UNIPROT:P21275; GB:L47480; NID:g994733; PIDN:AAC37698.1; PID:g99473
 R:Dickinson, M.E.; van der Meer-de Jong, R.; Hoggan, B.L.M.
 Submitted to the EMBL Data Library, December 1990
 A:Description: Nucleotide sequence of the mouse Bone Morphogenetic Protein-4 (BMP-4) cD.
 A:Reference number: S29523
 A:Accession: S29523
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 13-420 <DIC>
 A:Cross-references: EMBL:X56848; NID:g50180; PIDN:CAA40179.1; PID:g50181
 R:Dickinson, M.E.; Kobrin, M.S.; Silan, C.M.; Kingsley, D.M.; Justice, M.J.; Miller, D.
 peland, N.G.; Jenkins, N.A.
 Genomics 6, 505-520, 1990
 A:Title: Chromosomal localization of seven members of the murine TGF-beta superfamily s
 A:Reference number: A34201; PMID:90228966; PMID:1970330
 A:Accession: B34201
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr
 A:Molecule type: mRNA
 A:Residues: 253-420 <DI2>
 C:Genetics:
 A:Gene: BMP-4
 A:Introns: 11/1; 13/7/1
 C:Superfamily: inhibin

Query Match 39.9%; Score 351; DB 2; Length 420;
 Best Local Similarity 48.1%; Pred. No. 1.2e-21;
 Matches 64; Conservative 19; Mismatches 32; Indels 18; Gaps 2;

QY 46 GGAGRGH-----GRRGRSRSRKSILHYDFKELGMDMTIAPLDYEAYH 88
 DB 289 GHGGRGHTLRRRAKSPKHHSGRAKKKNCRRHSLYDFSGVGNMDIIVAPRGYQAF 348
 QY 89 CEGVCDPFLRSHLEPTNHAIIQTLLNSMAPDAAPASCVPARLSPISIIYIDANNVYK 148
 DB 349 CHGDCPFLADHINSTNHAIVQTLVNSV-SSIFPKACVPTLSAISMLYIDEDYKVL 407

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OM protein - protein search, using SW model

Run on: July 15, 2005, 15:06:06 ; Search time 163 Seconds

(without alignments)
382.146 Million cell updates/sec

Title: US-10-758-210-6

Perfect score: 880
Sequence: 1 AGSRKANLGGRRRRRTALAG.....ANNVVYQYEDMVVEAGCR 161

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1729182 seqs, 38693608 residues

Total number of hits satisfying chosen parameters: 1729182

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	880	100.0	161	US-10-758-210-6	Sequence 6, Appl1
2	862	98.0	240	US-09-945-182-30	Sequence 30, Appl1
3	830	94.3	151	US-10-164-279-61	Sequence 61, Appl1
4	712.5	81.0	294	US-09-945-182-2	Sequence 2, Appl1
5	712.5	81.0	388	US-09-945-182-34	Sequence 34, Appl1
6	712.5	81.0	388	US-10-366-345-43	Sequence 43, Appl1
7	712.5	81.0	450	US-10-188-246-12	Sequence 12, Appl1
8	712.5	81.0	450	US-10-481-698-18	Sequence 18, Appl1
9	682.5	77.6	411	US-09-945-182-28	Sequence 28, Appl1
10	657	74.7	119	US-10-758-210-7	Sequence 7, Appl1
11	563	64.0	104	US-10-366-345-68	Sequence 68, Appl1

	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	
	556	554	553	553	553	553	553	551	544	540.5	540.5	540.5	540.5	540.5	540.5	540.5	536	535	533	526	512	510	510	510	510	510	508.5	508.5	502	502	502	502	498.5	498.5	
	63.2	63.0	62.8	62.8	62.8	62.8	62.8	62.6	61.8	61.4	61.4	61.4	61.4	61.4	61.4	61.4	60.9	60.8	60.6	59.8	58.2	58.0	58.0	58.0	58.0	58.0	57.8	57.8	57.0	57.0	57.0	57.0	56.6	56.6	
	134	354	321	321	321	321	321	263	412	436	436	436	436	436	436	436	413	413	413	495	8	8	8	8	8	8	16	16	119	9	9	9	9	9	9
	US-10-693-536-6	US-09-930-512-74	US-09-945-182-26	US-10-366-345-44	US-09-825-751A-20	US-09-930-512-20	US-10-297-639-6	US-09-945-182-32	US-09-930-512-75	US-09-730-772-14	US-09-735-849-14	US-09-825-751A-85	US-09-574-819-14	US-09-930-512-72	US-10-379-830-14	US-10-164-279-57	US-10-693-536-7	US-09-930-512-73	US-10-166-345-69	US-09-930-512-76	US-09-880-708-10	US-08-981-490B-1	US-10-164-279-53	US-10-356-513-1	US-10-356-513-5	US-09-813-398-37	US-10-826-324-37	US-08-945-459A-1	US-09-880-708-13	US-09-068-253-2	US-10-365-231-1	US-09-945-182-4	US-09-730-772-13	US-09-735-849-13	
	Sequence 6, Appl1	Sequence 74, Appl1	Sequence 26, Appl1	Sequence 44, Appl1	Sequence 20, Appl1	Sequence 20, Appl1	Sequence 6, Appl1	Sequence 32, Appl1	Sequence 75, Appl1	Sequence 14, Appl1	Sequence 14, Appl1	Sequence 85, Appl1	Sequence 14, Appl1	Sequence 72, Appl1	Sequence 14, Appl1	Sequence 57, Appl1	Sequence 7, Appl1	Sequence 73, Appl1	Sequence 69, Appl1	Sequence 76, Appl1	Sequence 10, Appl1	Sequence 1, Appl1	Sequence 53, Appl1	Sequence 1, Appl1	Sequence 5, Appl1	Sequence 37, Appl1	Sequence 37, Appl1	Sequence 1, Appl1	Sequence 13, Appl1	Sequence 2, Appl1	Sequence 4, Appl1	Sequence 13, Appl1	Sequence 13, Appl1		

ALIGNMENTS

RESULT 1
US-10-758-210-6
Sequence 6, Application US/10758210
Publication No. US20040127696A1
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: LEE, Se-jin
TITLE OF INVENTION: ANTIBODIES BINDING TO GROWTH DIFFERENTIATION FACTOR-7
FILE REFERENCE: JHU130-2
CURRENT APPLICATION NUMBER: US/10/758,210
CURRENT FILING DATE: 2004-01-14
PRIOR APPLICATION NUMBER: US/09/412,791D
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/581,528
PRIOR FILING DATE: 1996-01-09
PRIOR APPLICATION NUMBER: PCT/US94/07799
PRIOR FILING DATE: 1994-07-08
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 161
TYPE: PRT
ORGANISM: Mus musculus
US-10-758-210-6

Query Match 100.0%; Score 880; DB 16; Length 161;
Best Local Similarity 100.0%; Pred. No. 5, 1e-54;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 AGSRKANLGGRRRRRTALAGTGAQGGGGGGGGGGGGGGGAGRGHGRSRRC 60
Db 1 AGSRKANLGGRRRRRTALAGTGAQGGGGGGGGGGGGGGGAGRGHGRSRRC 60

Qy	Db	Qy	Db
6	61	121	121
SRSLHYDFEALGMDMMIAPLDYEAHYHGGVCDPLRSHLEPTNHAITQTLNLSMPDA	SRSLHYDFEALGMDMMIAPLDYEAHYHGGVCDPLRSHLEPTNHAITQTLNLSMPDA	APASCCVPARLSPSTILYTDAAANNVYKQYEMVYEAACGR	APASCCVPARLSPSTILYTDAAANNVYKQYEMVYEAACGR
120	120	161	161

RESULT 2

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US-09-945-182-30
? Sequence 30. Application US/09945182
? Patent No. US2002016094A1
? GENERAL INFORMATION:
? APPLICANT: Celeste, Anthony J.
?           Wozney, John
?           Rosen, Vicki A.
?           Wolfman, Neil
?           Thomsen, Gerald H.
?           Melton, Douglas A.
? TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
? NUMBER OF SEQUENCES: 35
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: GENETICS INSTITUTE, INC.
? STREET: 87 CambridgePark Drive
? CITY: Cambridge
? STATE: Massachusetts
? COUNTRY: USA
? ZIP: 02140
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent in Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/945,182
? FILING DATE: 31-Aug-2001
? CLASSIFICATION: <Unknown>
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/808,324
? FILING DATE: <Unknown>
? ATTORNEY/AGENT INFORMATION:
? NAME: Lazar, Steven R.
? REGISTRATION NUMBER: 32,618
? REFERENCE/DOCKET NUMBER: 5202-D
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 617 498-8260
? TELEFAX: 617 876-5851
? INFORMATION FOR SEQ ID NO: 30:
? SEQUENCE CHARACTERISTICS:
?   LENGTH: 240 amino acids
?   TYPE: amino acid
?   TOPOLOGY: linear
? MOLECULE TYPE: protein
? SEQUENCE DESCRIPTION: SEQ ID NO: 30:
? US-09-945-182-30

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Query Match	98.0%	Score 862;	DB 9;	Length 240;
Best Local Similarity	97.5%	Pred. No. 1.2e-52;		
Matches 157;	Conservative 1;	Mismatches 3;	Indels 0;	Gaps 0.
QY	1	AGSRKANLGGRRRRRTALATRGAGSGSGGGGGGGGGGGGGGGGAGRGHGRGRRC	60	
		:		
Db	80	AGSRKANLGGRRRQRTALATRGKXGSGGGGGGGGGGGGGGGGGGAGRGHGRGRRC	139	
QY	61	SRKSLAVDFKELGMDWIIAPLDYEAHCEGVCFPLRSHLEPTNHAIIQTLLNSMAPDA	120	
Db	140	GRKSLHDFKELGMDWIIAPLDYEAHCEGVCFPLRSHLEPTNHAIIQTLLNSMAPDA	199	
QY	121	APASCCVAPARLSPISILYTDANNVYVQYEDMVVEAGCR	161	
Db	200	APASCCVAPARLSPISILYTDANNVYVQYEDMVVEAGCR	240	

RESULT 3
 US-10-164-279-61
 ; Sequence 61, Application US/10164279
 ; Publication No. US20030185792A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Keck, P.
 ; TITLE OF INVENTION: MORPHOGEN ANALOGS OF BOND MORPHOGENIC PROTEINS
 ; FILE REFERENCE: CIBT-P04-566
 ; CURRENT APPLICATION NUMBER: US/10/164,279
 ; CURRENT FILING DATE: 2002-06-06
 ; PRIOR APPLICATION NUMBER: 09/791946
 ; PRIOR FILING DATE: 2001-02-22
 ; NUMBER OF SEQ ID NOS: 64
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 61
 ; LENGTH: 151
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; US-10-164-279-61

Query Match	94.3%	Score 830	DB 14	Length 151
Best Local Similarity	100.0%	Pred. No. 1.5e-50		
Matches 151	0	Mismatches 0	Indels 0	Gaps 0
Conservative				

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Oy      11 RRRRTALTAGTGAAGSGGGGGGGGGGGGGGAGRGHRGRGRCSRSKSLHVDPK 70
         |||||
Db      1 RRRRTALTAGTGAAGSGGGGGGGGGGGGGGAGRGHRGRGRCSRSKSLHVDPK 60

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QY      71 ELGMDMWIAPLDYEAYHCEGCDEPLRSHEPTNNAIQTLNSMAPDAAPASCCVPAR 130
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DB      61 ELGMDDWIAPLDYEAYHCEGCDEPLRSHEPTNNAIQTLNSMAPDAAPASCCVPAR 120
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Qy      131 LSPISILYIDAANNVYKQEDMVVEACGCR 161  
        |||||  
Db      121 LSPISILYIDAANNVYKQEDMVVEACGCR 151
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RESULT 4

US-09-945-82-2
Sequence 2, Application US/09945162
Patent No. US20020160494A1
GENERAL INFORMATION:
APPLICANT: Celeste, Anthony J.
Wozney, John
Rosen, Vicki A.
Wolfman, Neil
Thomsen, Gerald H.
Melton, Douglas A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENETICS INSTITUTE, INC.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/945,162
FILING DATE: 31-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/808,324
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618

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1      REFERENCE/DOCKET NUMBER: 5202-D
2      TELECOMMUNICATION INFORMATION:
3      TELEPHONE: 617 498-8260
4      TELEFAX: 617 876-5851
5      INFORMATION FOR SEQ ID NO: 2:
6      SEQUENCE CHARACTERISTICS:
7      LENGTH: 294 amino acids
8      TYPE: amino acid
9      TOPOLOGY: linear
10     MOLECULE TYPE: protein
11     SEQUENCE DESCRIPTION: SEQ ID NO: 2:
12     US-09-945-182-2
13
14     Query Match      81.0%; Score 712.5; DB 9; Length 294;
15     Best Local Similarity 84.9%; Pred. No. 3,7e-42;
16     Matches 135; Conservative 3; Mismatches 4; Indels 17; Gaps 1.
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[illegible]

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? PRIOR FILING DATE: 2002-07-03
? PRIOR APPLICATION NUMBER: US 60/303,500
? PRIOR FILING DATE: 2001-07-05
? PRIOR APPLICATION NUMBER: US 60/305,403
? PRIOR FILING DATE: 2001-07-13
? PRIOR APPLICATION NUMBER: US 60/307,011
? PRIOR FILING DATE: 2001-07-20
? PRIOR APPLICATION NUMBER: US 60/308,187
? PRIOR FILING DATE: 2001-07-27
? PRIOR APPLICATION NUMBER: US 60/309,416
? PRIOR FILING DATE: 2001-08-01
? PRIOR APPLICATION NUMBER: US 60/311,740
? PRIOR FILING DATE: 2001-08-09
? PRIOR APPLICATION NUMBER: US 60/343,553
? PRIOR FILING DATE: 2001-12-21
? NUMBER OF SEQ ID NOS: 62
? SOFTWARE: PERL Program
? SEQ ID NO 18
? LENGTH: 450
? TYPE: PRT
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: misc_feature
? OTHER INFORMATION: Incyte ID No: 748635ICD1
US-10-481-698-18

Query Match      81.0%; Score 712.5; DB 16; Length 450;
Best Local Similarity 84.9%; Pred. No. 5,2e-42;
Matches 155; Conservative 3; Mismatches 4; Indels 17; Gaps 1

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Db      352  KPLAHVDKFKLGMDDMIITAPLDVEAHGCGCDFPLRSLTEPTNNAIIQTLLNSWAPAP 411
Qy      123  ASCCVPARLSPISILYIDANNVYKQYEDMWVEACGR 161
      |||||
Db      412  ASCCVPARLSPISILYIDANNVYKQYEDMWVEACGR 450

```

Mooney, John
Rosen, Vicki A.
Wolfman, Neil
Thomson, Gerald H.
Melton, Douglas A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSER: GENETICS INSTITUTE, INC.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/945,182
FILING DATE: 31-Aug-2001
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:

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